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using sw model - protein search, OM protein

November on: Run

9, 2004, 11:57:37; Search time 27.25 Seconds (without alignments) 4014.622 Million cell updates/sec

US-09-902-481B-3 Perfect score: Title:

1 FNLDTENAMTFQENARGFGQ.....FKRQYKDMMSEGGPPGAEPQ 1137 Sequence:

BLOSUM62 Gapop 10.0 , Gapext Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 DB DB Maximum Maximum

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\* .. .. ..

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description           |        | <u>ذر ا</u><br>د ا | canocyce sur | 1 [    | umphograph fr | בייטטין<br>קייטטין ר | d plud e | alpha<br>alpha | dipin hom | rrin almha-2 | Thha-1 | - Donor |        | 1 pira - 4 | י הלמנה | a Pila |        | ace    | alpha subun<br>rin aleka f | alpha-5 |        | integrin alpha-v c | rin ro | rin recep | alpua-6 |        | arpna-3 | alpha- | ι.<br>Ε. |
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| SUMMARIES | ID                    | RWHUIB | 800551             | . :          | 803308 | 156126        | A53213               | A45226   | 145914         | S44142    | 3399         | A35854 | A41131  | S06046 | 10         | T31437  | JC7294 | A35761 | I55534 | S44250                     | A36108  | T10050 | A38457             | A27079 | 542       | 2742    | $\sim$ | 4154    | 1651   | A29637   |
|           | DB                    | 1      | 7                  | Н            | ~      | ~             | 7                    | 7        | 7              | 7         | 7            | ~      | 7       | ~      | ~          | 7       | N      | (7)    | N      | N                          | ~       | 7      | 7                  | ~      | 7         | 7       | 2      | ~       | 1 00   | 7        |
|           | Query<br>Match Length | 11     | ⊣                  | 16           | 1170   | 1163          | 1179                 | 1151     | 1170           | 1178      | 1181         | 1180   | 1039    | 1038   | 1035       | 1041    | 1054   | 1051   | 1053   | 1053                       | 1034    | 1044   | 0                  | 04     | 07        | 04      | 05     | 60      | 1044   | 39       |
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|           | Score                 | 5839   | 4447               |              |        | 1516.5        | 1128                 | u)       | 1071           | $\circ$   | $^{\circ}$   | 0      | 999     | 642    | 630        | 614.5   | 579.5  | 572.5  | 567.5  | 555.5                      | 551.5   | 539    | 533.5              | 532    | 531       | 530     | 529.5  | 524.5   | 514.5  | 497      |
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| 840311             | 775950            | 161186             | A60163       | B30892             | S38783             | S44824          | S60571           | S28277             | T09403             | T09433             | 136916          | T18523             | 136917           | A55348             |
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| 8 a                | 0 00              | 8.3                | 8.3          | 8.3                | 8.0                | 7.9             | 7.8              | 7.6                | 7.1                | 7.0                | 6.7             | 5.3                | 5.1              | 4.8                |
| 496.5              | 491               | 490                | 487.5        | 486                | 470                | 466             | 458.5            | 444.5              | 418                | 413.5              | 391             | 309                | 299              | 279.5              |
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## ALIGNMENTS

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A,Reference number: A31108; MUID:88315033; PMID:2457584
A,Accession: A31108
A,Accession: A31108
A,Accession: A31108
A,Roclecule type: MRNA
A,Residues: 1-1153 <COR>
A,Cross-references: UNIPROT:P11215, GB:J03925; NID:g187284; PIDN:AAA59544.1; PID:g307148
A,Radout, M.A.; Gupta, S.K.; Pierce, M.W.; Tenen, D.G.
J. Cell Biol. 106, 2153-2158, 1988
A,Fitle: Amino acid sequence of the alpha subunit of human leukocyte adhesion receptor y A,Recession: A28915; MUID:88257215; PMID:2454931
A,Accession: A28915; MUID:88257215; PMID:2454931
A,Rocles in A28915; MUID:88257215; PMID:2454931
A,Rocles in A28915; MUID:88257215; PMID:2454931
A,Rocles in A28915; MUID:8927215; PMID:2454931
A,Rocles in A1499; S01-965, 'P., 967-1153 <ARN>
A,Cross-references: GB:M18404; GB:J03270; GB:M19664; GB:X07421; NID:g186935; PIDN:AAA594
A,Cross-references: GB:M18404; GB:J03270; GB:M19664; GB:X07421; NID:g186935; PIDN:AAA594
A,Rocles in Adding the codon TAC for residue 1129 as Thr
B,Shelley C. S.; Armaout, M.A.
A,Rocles in A1600
A,Rocles in A16

A; Molecule type: mRNA A; Residues: 917-1042 <AR2>

A.Cross-references: GB:M18044
R;Hickstein, D.D.; Hickey, M.J.; Ozols, J.; Baker, D.M.; Back, A.L.; Roth, G.J.
Proc. Natl. Acad. Sci. US.A. 86, 257-261, 1989
A;Title: cDNA sequence for the alpham subunit of the human neutrophil adherence receptor A;Reference number: A32218; MUID:89098893; PMID:2563162

A;Molecule type: mRNA A;Residues: 9-1153 <HIC> A;Cross-references: GB:J04145; NID:g189068; PIDN:AAA59903.1; PID:g386975

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NID:952982; PIDN:CAA30479.1; PID:95298 residue 569 as Gln
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NPEALKTVQNQLREKIFAIEGTQTGSSSSFEHEMSQEGFSAAITSNGPLLSTVGSYDWAG
                                                                                                                   QNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPL
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                                                                                      GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR
                                                                                                                                                                                                                                                                          PRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLF
                                                                                                                                                                                                                                                                                                                                                                        HGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTVGAQGHVLLLRSQ
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A,Molecule type: DNA
A,Residues: 1-1153 - 4PYT>
A,CSS-treferences: UNIPROT:P05555; EMBL:X07640; 1
A,Note: the authors translated the codon CAC for:
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       A;Note: part of this sequence was confirmed by protein sequencing
R;Fleming, J.C.; Pahl, H.L.; Gonzalez, D.A.; Smith, T.F.; Tenen, D.G.
J. Immunol. 150, 480-490, 1993
A;Title: Structural analysis of the CD11b gene and phylogenetic analysis of the alpha-in during evolution.
A;Gesenson: A46526, MUID:93123748; PMID:8419480
A;Accession: A46526, MUID:93123748; PMID:8419480
A;Accession: A46526
A;Status: not compared with conceptual translation
A;Accession: A65227; NID:9323047; PIDN:AAB24821.1; PID:9263049
A;Cross-references: GB:55227; NID:9263047; PIDN:AAB24821.1; PID:9263049
A;Cross-reference extracted from NGBI backbone (NCBIP:121963)
B;Picrce, M.W.; Remold-O'Donnell, E.; Todd III, R.F.; Arnaout, M.A.
B;Cocinim: Biophys. Acta 874, 368-371, 1986
A;Attle: N-terminal sequence of human leukocyte glycoprotein Mol: conservation across SpA;Accession: A26691
A;Accession: A26691
A;Accession: A26691
A;Accession: A26691
A;Accession: A26691
A;Accession: A26691
A;Accession: A26691
A;Attle: Nosmarin, A.G.; Tenen, D.G.
Blood 79, 865-870, 1992
A;Title: Characterization of the myeloid-specific CD11b promoter.
A;Reference number: 152567; MUID:92144986; PMID:1346576
A;Attle: Aracidated from GB;EMBL/DPBJ
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A;Crosereferences: GDB:120599; OMIN:120980
A;Crosereferences: GDB:120-16p11.2
A;Note: promoter contains a GATA motif and two Sp1 consensus binding sites
A;Note: promoter contains a GATA motif and two Sp1 consensus binding sites
A;Note: promoter contains a GATA motif and two Sp1 consensus binding sites
C;Supwords: alternative splicing; calcium; cell adhesion; glycoprotein; heterodimer; mag
C;Reywords: alternative splicing; calcium; cell adhesion; glycoprotein; heterodimer; mag
F;17-1153/Product: cell surface glycoprotein CD11b #status experimental <MAT>
F;17-1108/Domain: stracellular #status predicted <EXT>
F;17-1108/Domain: von Willebrand factor type A repeat homology <WMA2>
F;17-1108/Domain: von Willebrand factor type A repeat homology <WMA2>
F;530-538/Region: calcium/magnesium binding #status predicted
F;530-538/Region: calcium/magnesium binding #status predicted
F;1109-1134/Domain: transmembrane #status predicted <TWM>
F;1135-1153/Domain: intracellular #status predicted <INT>
F;135-1153/Domain: intracellular #status predicted <INT>
F;135-1153/Domain: intracellular #status predicted <INT>
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A;Molecule type: DNA
A;Residues: 1-9 <a href="https://document.nc.nd/">https://document.nd/</a>
A;Residues: 1-9 <a href="https://document.nd/">https://document.nd/</a>
A;Cromsont: A common beta chain (CD18) forms a heterodimer with this chain to form Mac-1
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Pred. No. 0;
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R;Sastre, L.; Roman, J.M.; Teplow, D.B.; Dreyer, W.J.; Gee, C.E.; Larson, R.S.; Roberts, Proc. Natl. Acad. Sci. U.S.A. 83, 5644-5648, 1986
A;Title: A partial genomic DNA clone for the alpha subunit of the mouse complement recep A;Reference number: 159078; MUID:86287312; PMID:2942940
A;Accession: 159078
A;Accession: 159078
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Robecule type: DNA
A;Residues: 11-44 <RES>
A;Cross-references: GB:M14293; NID:g198993; PIDN:AA39484.1; PID:g554193
A;Genetics:
A;G
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75.6%; Score 4447; DB 2;
Best Local Similarity 73.5%; Pred. No. 9.6e-303;
Matches 836; Conservative 147; Mismatches 153;
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Best Local 9
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Cipperies: Homo sapiens (man)
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A.Recenter an Carcia-Agails; Goods di
A.Recenter an Carcia-Agails; U. 3: Springer, T.A.
A.Recenter brancher: A35584
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GPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLONQRSQRSWRL-ACESASSTE
                                    VSGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRTNKTE
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N'Alternate names: leukocyte adhesion receptor p150,95 alpha chain
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                                                                                        80 GLOVPPEAVNMSLGLSLASTISPSQLIACGPTVHHECGRNMYLTGLCFLLGPT--QLTQR
                                                                                                                                RLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLRQQPQK
                                                                                                                   PPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKELVSTIMEQLKKSKTLFSLMQYSEEF
                                     PNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQBIVAANQRGSLYQCDYSTGSCEPI
                  Gaps
                   9
 Length 1163;
                    Indels
58.8%; Score 3456; DB 1;
larity 60.6%; Pred. No. 2.5e-233;
Conservative 143; Mismatches 296;
             Similarity
                       684;
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Best Local S:
Matches 684
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Accession: Alone sapiene manes: leukocyte adhesion glycoprotein LFA-1 alpha chain; leukocyte function call surface glycoprotein CD11a precursor - human call surface glycoprotein CD1ate: 28-Feb-1990 #sequence revision 28-Feb-1990 #text_change 09-Jul-2004 C. Species: Home sapienes (man) A. Libate manes: leukocyte adhesion 28-Feb-1990 #text_change 09-Jul-2004 C. Date: 28-Feb-1990 #sequence revision 28-Feb-1990 #text_change 09-Jul-2004 C. Date: 28-Feb-1990 #text_change C. Date: 28-Feb-1990
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A/Map position: 16p11.2-16p11.2
C;Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat hom C;Keywords: cell adhesion; otycoskeleton; glycoprotein; heterodimer; surface antigen; t;F;1-25/Domain: signal sequence #status predicted <STG>
F;26-1170/Product: leukocyte adhesion glycoprotein LFA-1 alpha chain #status predicted F;154-317/Domain: von Willebrand factor type A repeat homology <VWA2>
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                                                                      1035 PSFSVQEELDFTLKGNLSFGWVRQILQKKVSVVSVAEITFDTSVYSQLPGQEAFMRAQTT 1094
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1020 PFFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLFGGGAFVRSQTE
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A;Gene: GDB:ITGAL; CD11A
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A; Residues: 1-20 <NUE>
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                                                                                                                                                                        XIHQVKHMYQVRIQPSIHDHNIPTLEAVVGVPQPPSEGPITHQWSVQMEPPV--PCHYED 1002
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                             KILFLLTDGEKFGDPLGYEDVIPELDREGVIRYVLGFGDAFRSEKSRQELNTVASKPPRD
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|XVLIIITDGE--ATDSGNIDAAKD----IIRYIIGIGKHFQTKESQETLHKFASKPASE
                                                                                       HVFQANNFEALKTVQNQLREKIFALEGTQTGSSSSFEHEMSQEGFSAALTSNGPLLSTVG
                                                                                                   SYDWAGGVF-LYTSKEKSTFINMTRVDSDMNDAYLGYAAA-IILRNRVQSLVLGAPRYQH
                                                                                                                                                                                                RGGOVSVCPLPRGQRARWQCDAV--LYGEQGQPWGRFGAALTVLGDVNGDKLTDVALGAP
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lymphocyte fuction-associated molecule-1-alpha - mouse C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 26-Uul-1996 #text_change 09-Jul-2004 C;Accession: 156126 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004 C;Accession: 156126 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004 J;Xaufmann, Y: Tseng, E.; Springer, T.A.
J. Immunol. 147, 369-374, 1991
A;Title: Cloning of the murine lymphocyte function-associated molecule-1 alpha-subunit A;Reference number: 156126 MUID:91268576; PMID:2051027 A;Accession: 156126 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: Infinary; translated from GB/EMBL/DDBJ
A;Residues: 1-1163 -RES>
A;Residues: 1-1163 -RES>
C;Genetics:
A;Gene: LFA-1
C;Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homotogy <WANI>F;151-315/Domain: von Willebrand factor type A repeat homology 
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....t.egrin alpha-1 chain - human (fragment)
C;Species: Homo sapiens (man)
C;Species: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Dacession: A45226
R;Briesewitz, R.; Epstein, M.R.; Marcantonio, B.E.
J. Biol. Chem. 268, 2989-2996, 1993
A;Title: Expression of native and truncated forms of the human integrin alpha 1 subuni
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                                                                                                                                                                                                                                                                                                                                       940 YQVSNLGQRSLPISLVFLVPVRLNQTVIWDRPQ----VTFSENLSS----TCHTKE-RLP 990
                                                                                                                                                                                                                                                             ELNGTVHCENENSSLQEDNSAATHIPVLYPVNILTKEQENSTLYISFTPKGPKTQQVQHV 947
                                                                                                                                                                                                                     LLKANVISEN-NMPRINKIEFQLELPVKYAVYMVVISHGVSIKYLNFIASENISRVMQHQ 939
                                                                                                                                                         -- PHSRMPVSCEEL--TEGSSLLIKTLKCNVSSPIFKAGQEVSLQVMFNTLLNSSWEDFV 887
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                                                                       QRSQRSWRLACESASSTEVSGAL-KSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKL
                                            ----REFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQN
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C;Genetics:
A;Gene: GDB:ITGAE
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Best Local Similarity 28.7%; Pred. No. 2.9e-70;
Matches 338; Conservative 213; Mismatches 454; Indels 172
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C;Superfamily: cell surface glycoprotein CD11b; von Willebrand
F;199-371/Domain: von Willebrand factor type A repeat homology
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A;Reference number: A45226; MUID:93155124; PMID:8428973
A;Accession: A45226
A;Accession: A5526
A;Scatus: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-1151 - SR1.>
A;Residues: MUIPROT:P56199
A;Residues: Sequence extracted from NCBI backbone (NCBIP:124326)
F;142-317/Domain: von Willebrand factor type A repeat homology <VWAL>
                                                                                                                                                                                        201;
                                                                                                                                                  Query Match 18.5%; Score 1085.5; DB 2; Length Best Local Similarity 27.6%; Pred. No. 2.6e-67; Matches 342; Conservative 209; Mismatches 488; Indels
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integrin PIDN:AAB59255.1; PID:g43969{ 970 PELKLSISFPNMTSNGYPVLYFTGLSS------SENANCRPHIFEDPFSINSGKK 1018 1031 TLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLPGQGAFVRSQTETKVEPFEVPNP 1090 ----OKRELAIQISKDGLPGR 1111 οĘ GALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGN-KLLLKANVTSENNMPRTNKTEF 900 911 NISIPVKYEVGLQFYS-SASEYHISIAANETVPEVINSTEDIGNEINIFYLIRKSGSFPM 969 48; 107 FLFGSNLRQQPQKFPBALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKELVSTIMEQLK-- 165 SDVSPDF-QLRISFAPAVQTCP-SFIDVVVVCDESNSIXPWD--AVKNFLEKFVQGLDIG 194 310 221 276 369 integrin alpha 2 subunit - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 16-Aug-1996 #sequence\_revision 16-Aug-1996 #text\_change 09-Jul-2004
C;Accession: 145914
R;Kamata, T.; Puzon, W.; Takada, Y.
D;Biol. Chem. 269, 9659-9663, 1994
A;Title: Identification of putative ligand binding sites within the I-domain A;Reference number: A54402; MUID:94193647; PMID:7511592
A;Accession: 145914
A;Status: preliminary; translated from GB/EMBL/DDBJ 54 78 EGFSAAIT--SNGPLLSTVGSYDWAGGVFLYTSKEKSTFINMT--RVDSDMN-DAYLGYA 391 | :: :::|: ---HLKRGTILLDCNTCKFATITCNLTSSDISQVNVSLILWKPTFIKSYFSSLNL 1 FNLDTENAMIFQ-ENARGFGQSVVQL---QGSRVVVGAPQEIVAANQRGSLYQC--DYST 55 GSCEPIRLQ-----VPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLC KSKTLFSLMQYSEEFRIHFTFKBFQNNPNPRSLIKPITQLL----GRTHTATGLRKVVRE 222 LFNITNGARKNAFKILFLLTDGEKFGDPLGYEDVIPELDREGVIRY---VLGF--GDAFR TKNLIKEIKAIASIPTERHFFNVSDBADLLEKAGTIGEQIFSIEGTVQG-GDNFQMEMSQ SEKSROELNTVASKPPRDHVFQANNFEALKTVQNQLREKIFAIEGTQTGSSSSFEHEMSQ A,Molecule type: mRNĀ A;Residues: 1-1170 «KAM» A;Cross-references: UNIPROT:PS3710; GB:L25886; NID:g439695; PIDN:AAB5 F;161-336/Domain: von Willebrand factor type A repeat homology «VWA2» Indels 168; --LPISLVF-----LVPVRLNQTVIWDRPQVTFSENLSSTCHTKE-Length 1170; QLELPVKYAVYMVVTSHGVSTKYLNFTASENTSRVMQHQYQVSN-1091 LPL--IVGSSVGGLLLLALITAALYKLGFFKRQYKDMMSE 1128 LPSHSDFLAELRKAPVVNCSIAVCQRIQCDIPFFGIQE--Query Match
18.2%; Score 1071; DB 2;
Best Local Similarity 27.5%; Pred. No. 2.8e-66;
Matches 334; Conservative 218; Mismatches 495; 1076 TIRGEL-----RSENASLVLSSSN----MTTSTD-686 1019 950 901 108 139 277 166 311 337 ð Db 8 g  $\delta$ qq ò В οp à à Db g ∂ à d  $\delta$ Dp ò qq ò q à 셤 à

Tue Nov

| VKGTQIGAYFGASL 445   | g                  | 370 VGFSABYSPQNNILMLGAVGAYDWSGTVVQKTPHGHLIFSKQAFEQILQDRNHSSYLGYS 429 | A,Cross-reference<br>F:169-344/Domain | ere   |
|--|--------------------|--|---------------------------------------|-------|
| 4.0 VASISTORGENUTUATION TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO | λ                  | AAIILRNRVQSLVLGAPRXQHIGLVAMFRQNTGMWESNANVKGTQIGAYFGASL 44            | Ouerv Mat                             | ch    |
| CONTRINCED   CONTRICTOR   CONTRINGED   CONTRIGION   CON   | op qu              | VASISTGNSVHFVAGAPRANYTGQIVLYSVNENGNVTVIQSQRGDQIGSYFGSVL              | Best Loca<br>Matches                  | 341;  |
| -IIANWHOFLEGPNGLENA 541  SGSGISPSHSQRIAGSKL 561  CMILLAPSQXILGSDRAF 600  DDCARPHERNAVP 621  CMSGRPHSRAVPN 677  CMCARPHERNAVP 677  CMCARPELSARVIN 677  CMCARPELSARVIN 677  CMCARPELSARVIN 677  CMCARPELSARVIN 677  CMCARPELSARVIN 733  CMCARPELSA   | ٥٧                 | CSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPLPRGRARWQCDAVLYGEQGQPWG            | λŏ                                    |       |
| ### SEGGISPERSORIAGS - KL 561  ### Signature   | qu                 | CAVDVNKDTITDVLLVGAPMYMNDLKKEEGRVYLFTITKG-ILNWHOFLEGPNGLENA           | Db                                    | 27 YN |
| EGW-IRLRYSOKILGSDRAF 600  ULRUVARIMENPREVARNY 621  | ٥y                 | RFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKL           | δλ                                    | 55    |
| 1  | qq                 | RFGSAIRALSDINMDGFNDVIVGSPLENQNSGAVYIYNGHEGM-IRLRYSQXILGSDRAF         | qa                                    | 87    |
| TADDYSVDASFTEKKITLL 658  | δλ                 | SPRLQYFGQSLSGGQDLTMDGLVDLTVGAQGHVLLLKSQPVLRVKAIMEFNPREVARNVF         |                                       | 108   |
| DALDSGRPHSRAVEN 677  | qq                 | SSHLOYFGRSLDGYGDLNGDSITDVSVGAFGQVVQLMSQSIADVSVDASFTPKKITLL           |                                       | 147   |
| THILDEDGESSRVISRGLEK 707  THILDEDGESSRVISRGLEK 707   | δλ                 | ECHDQVVKGKERAGEVRVCLHVQKSTRDRLREGQIQSVVTYDLALDSGRPHSRAVFN            |                                       | 165   |
| ### TRIANESIT VGTPLSAFGNL 733  | qq                 | NKNAEIKLKLCFSAKFRPTNQNNQVAIVYNITIDEDQFSSRVISRGLFK                    |                                       | 200   |
| ### A CONTRINITY AND THE PRINCE TO THE PRINCE OF THE PRINC | δý                 | ETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNFSLVGTPLSAFGNL             |                                       | 222   |
| SFMSIDCLVVGGPREFNUTY 789   | Db                 | ENNERCLOKTMIVSQAQRCSEYIIHIQEPSDIISPLNLCMNISLENPGT                    | qa                                    | 260   |
| ### SETONORMERLTESN 816  ### SETONORMERLTESN 816  ### SETONORMERLTESN 816  ### SETONORMERLTESN 816  ### SETONORMERLESN 816  ### SETONORMERLESN 813  ## | ΟY                 | RPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVGGPREFNVTV             | λō                                    | 277   |
| ### SERVICE STATE  | qq                 | NPALEAYSETVKVFSIPFHKDCGDBGVCISDLVLNVQQLPATQQQPFIVSNQNKRLTFSV         | qq                                    | 319   |
| ### SEND CONTRINGUE NOT  | δy                 | TVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASST-EVSGALKSTS         | λŏ                                    | 337   |
|  | Д                  | QIKNKKESAYNTEIVVDFSENLFFASWSMPVDGTEVTCQIASSQKSVT                     | QO                                    | 378   |
| ## SEQUEENMADNSVNLKLSLIX 923  ## PROTECTION NOT BE   | ò                  | CSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRTNKTEFQLELPVKY         | ζŎ                                    | 392   |
| ### STATE OF THE PROPERTY AND THE PROPERTY OF THE PRINCIPLE OF THE PROPERTY OF THE PRO | οp                 | CNVGYPALKSKQQVTFTINFDFNLQ-NLQNQASISFRALSESQEENMADNSVNLKLSLLX         | qα                                    | 438   |
| KETESIKVTTGSVPVSMA 976  DD RLPEHSDFLAE- 998  ABINPLKIGGTSSSVSFKSEN 1030  BD  FDWYIKTSHNHLLIVSTAEI- 1057  NGTFAASTFCTVQLTAAAEID 1090  PLDLIVGSSVGGLLLLALITA 1110  CAY  PTGVIVGSVIAGILLLALITA 1110  CAY  PTGVIVGSVIAGILLLALITA 1140  DD  CAY  WANG, D.Z.; Damjanovich, L.; Latze  DD  CAY  Wang, D.Z.; Damjanovich, L.; Latze  DD  OY  Wang, D.Z.; Damjanovich, DD  DD   | δλ                 | AVYMVVTSHGVSTKYLNFTASENTSRVMCHQYQVSNLGQRSLPISLVFLV                   | ۸ö                                    | 448   |
| ### ABLINPLANG   198   20  | Db                 | DAEIHIT-RSTNINFYEVSLDGNVSSVV-HSFEDIGPKFIFSIKVTTGSVPVSMA              | qQ                                    | 495   |
| ABINPLKIGGTSSSVSFKSEN 1030  EDMYIKTSHNHLLIVSTABI- 1057  S.:.:      NGTFAASTFGTVGLTAAABID 1090  PLPLIVGSSVGGLLLLALITA 1110  PTGJVIVGSVIAGILLLALITA 1140  Db  ext_change 09-Jul-2004  Wang, D.Z.; Damjanovich, L.; Latze  Db  Oy  Wang, D.Z.; Damjanovich, L.; Latze  Db  Oy  Oy  Wang, D.Z.; Damjanovich, L.; Datze  Oy  Oy  Oy  Oy  Oy  Oy  Oy  Oy  Oy  O  | ò                  | PVRLNQTVIWDRPQVTFSENLSSTCHTKE  | δλ                                    | 909   |
| FDWYIKTSHNHILIVSTREI- 1057  NGTFAASTECTVQLTAAAEID 1090  PLPLIVGSSVGGLLLALITA 1110  QY  PTGVIVGSVIAGILLLALITA 1140  Db  QY  Ext_change 09-Jul-2004  Wang, D.Z.; Damjanovich, L.; Latze  Db  QY  Wang, D.Z.; Damjanovich, L.; Latze  Db  Oy  Wang, D.Z.; Damjanovich, L.; Latze  Db  | Dp                 | SVIIHIPQYTKDKNPLMYLTGVHTDQAGDISCEAEINPLKIGQTSSSVSFKSEN               | ପ୍ପ                                   | 552   |
| NGTFAASTFQTVQLTAAAEID 1090  PLPLIVGSSVGGLLLAALITA 1110  QY  PTGVIVGSVIAGILLLALVA 1140  Db  GX  ext_change 09-Jul-2004  Wang, D.Z.; Damjanovich, L.; Latze  Db  Cy  Oy  Db  Qy  Db  Qy  Db  Qy  Wang, D.Z.; Damjanovich, L.; Latze  Db  | ò                  | LRKAPVNICSIAVCQRIQCDIPFFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEI-         | ò                                     | 565   |
| PLPLIVGSSVGGLLLALITA 1110  | qq                 | FRHIKELNÖRTÄSCSNIMÖWLRDLQVKGEYFLNVSTRIWNGTFAASTFQTVQLTAAAEID         | qq                                    | 611   |
| prGVIVGSVIAGILLILALVA 1140  Db  Qy  Ext_change 09-Jul-2004  Wang, D.Z.; Damjanovich, L.; Latze  Db  Lagen and laminin adhesion but not  Db   | δλ                 | LENDSVETLLPGQGAFVRSQTETKVEPFE-VPNPLPLIVGSSVGGLLLALITA                | δλ                                    | 624   |
| ext_change 09-Jul-2004  Wang, D.Z.; Damjanovich, L.; Latze Db Lagen and laminin adhesion but not Db  | Db                 | TYNPQIYVIBENTVTIPLTIMKPHEKVEVPTGVIVGSVIAGILLLLALVA                   | QQ                                    | 661   |
| ext_change 09-Jul-2004  Wang, D.Z.; Damjanovich, L.; Latze Db  Lagen and laminin adhesion but not Db  Oy  Oy  Oy   | δy                 | ALYKLGFFKRQYKDM 112  | δλ                                    | 680   |
| ext_change 09-Jul-2004  Wang, D.Z.; Damjanovich, L.; Latze  Db  Lagen and laminin adhesion but not  Db   | Dp                 | ILWKLGFFKRKYEKM 115  | qa                                    | 718   |
| Db Wang, D.Z.; Damjanovich, L.; Latze Db Lagen and laminin adhesion but not Db   | RESULT             | o  | 6                                     | 738   |
| wang, D.Z.; Damjanovich, L.; Latze Db Wang, D.Z.; Damjanovich, L.; Latze Db Lagen and laminin adhesion but not Db Db   | S44142<br>VLA-2    | protein homolog - mouse  | QQ                                    | 769   |
| Wang, D.Z.; Damjanovich, L.; Latze Db. Lagen and laminin adhesion but not Db Db  | C;Spec<br>C;Date   | .ext_change  | λο                                    | 789   |
| lagen and laminin adhesion but not Oy  Db  | C; Acce<br>R; Edel | Wang, D.Z.; Damjanovich, L.; Latz                                    | Db                                    | 824   |
| da<br>Vo   | submit<br>A:Desc   | lagen and laminin adhesion but                                       | λŏ                                    | 848   |
| 70   | A; Refe            | rence number: S44142<br>ssion: S44142                                | qq                                    | 872   |
|  | A;Stat<br>A;Mole   | us: preliminary<br>cule type: mRNA                                   | ď                                     | 906   |

ces: UNIPROT: Q62469; EMBL: Z29987; NID: g473098; PIDN: CAA82877.1; PID: g4730 n: von Willebrand factor type A repeat homology <VWA2> 905 VKXAVYMVVTSHGVSTKYLNFTASENTSRVMQHQYQVSNLGQR------SLPISLV 955 VIVRNDGEDSYRIQVIFFFPLDLSYRKVSTLONQRSORSWRLACESASST-EVSGALKST 847 AEDAQRIFTALFPFEKNCGNDNICQDDLSI-----TFSFMSLDCLVVGGPREFNVT 788 | ::| || :| || || || || :| || :| || VILKNRGESAYNTVVLAEFSENLFF-----ASFSMPVDGTEVTCEVGSSQKSV 871 505 610 623 619 737 SERFLOKNMVVNEVQKCSEHHISIQKPS-----PAL 768 EAYSETVKVFSIPFYKEGGSDGICISDLILDVQQLPAIQTQSF-----IVSNQNKRLTFS 823 SGFSA--AITSNGPLLSTVGSYDWAGGVFLYTSKEKSTFINMT--RVDSDMN-DAYLGYA 391 447 564 JENITNGARKNAFKILFLLIDGEKFGDPLGYEDVIPELDREGVIRY---VLGF--GDAFR 276 SEKSRQELNTVASKPPRDHVFQANNFEALKTVQNQLREKIFALEGTQTGSSSSFEHEMSQ 336 437 494 551 TCEKLNLONDASISNVTBIKTNMSLGLTLTRNPGTGGFLTCGPLWAHQCGNQYYATGIC 146 107 LFGSNLRQQPQ----KFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKELVSTIMEQL 164 C--KSKILFSLMQYSEBFRIHFTFKEFQNNPNPRSLIKPITQLLG-RIHTATGLRKVVRE 221 SCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRINKTE--FQLELP NDQVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVTYDLALD----SGRPHSRAVFNET VDVDSNGSTDLVLIGAPHYYEQTR--GGQVSVCPLPRGQRARWQCDAVLYGEQGQPWGRF SAALIVI,GDVNGDKLIDVAIGAPGEEDNRGAVYLFHGISGSGISPSHSORIAGSKLSPR--LQYFGQSLSGGQDLTMDGLVDLTVGAQGHVLLLRSQPVLRVKAIMEFNPREVARNVFEC KNSTRRQTQVLGLTQTCET--LKLQLPNCIEDPVSPIVLRLNFSLVGTPLSAFGNLRPVL ALILENRVQSLVLGAPRYQHIGLVAMFRQNTGMWESNANV----KGTQIGAYFGASLCS SCEPIRLO------VPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLC NLDTENAMTFQ-ENARGFGQSVVQL---QGSRVVVGAPQEIVAANQRGSLYQC--DYST Gaps 18.0%; Score 1057; DB 2; Length 1178; .larity 27.8%; Pred. No. 2.7e-65; Conservative 209; Mismatches 487; Indels 188; 

|      | 722 ERCLÖKUM'VNOAÖSTPEHIIYIÖEFSDVNNSLDLKUDISLENPGTSPALE 772 739 EDAQRLFTALFPFEKNCGNDNICQDDLSITFSEMSLDCLVVGGPREFNVTVTVRND 794 773 AYSETAKVFSIPPHKDGGEDGLCISDLVLDVRQIPAAQEQPFIVSNQNKRLTFSVTLKKK 832 795 GEDSYRTQVTFFPPLDLSYRKVSTLQNORSQRSWILACESASST-EVSGALKSTSCSINH 853 833 RESAYNTGIVVDFSENLFFASFSLPVDGTEVTCQVAASQKSVACDVGY 880 854 PIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRTNKTFFOLELPVKXAVYWV 913 881 PALKREQVYTFTINFDFNLO-NIQNQASLSFQLSSQEBNKADNLVNLKIPLLYDASI- 938 914 VTSHGVSTKYLNFTASENTSRVMQHOYQVSNLGQRSLPISLVFLLYDASI- 938 915HLTRSTNINFYEISSDGNVFSIVHSFEDVGPKFIFSLKVTTGSVPVSMATVIHIPQ 995 916 VTKEKNPLMXLTGVQFDKAGDISCNADINPLKIGQTSSSVSFKSENFRHTKE- 1047 917 SHGVSTKXLNNFYEISSDGNVFSIVHSFEDVGPKFIFSLKVTTGSVPVSMATVIHIPQ 995 918 LPSHSDFLAELRKAPVVNCSIAVCQRIQCDIPFGIQBERNATLKGNLSFDMYIKTSHNH 1048 1048 |
|------|---|
| 2 ch | negati Db Oy alent) Db Oy  |
|      | 18-21 < 2UT)  18-21   |

| Qy 614 REVARNVEECNDQVVKGKEAGEVRVCLHVQ-KSTRDRLREGQIQSVVTYDLALDSGRP 670    :     :       :                      |  | RESULT 12  Ayalla  Ayalla  Iymphocyte-Peyer's patch adhesion molecule alpha 4 precursor - mouse  NyAlternate names: integrin alpha-4  C;Species Ma musculus (house mouse)  C;Date: 05-Jun-1992 #sequence_revision 05-Jun-1992 #text_change 09-Jul-2004  C;Datcesion: Alla1; Sid742  C;Accession: Alla1; Sid742  A;Neuhaus, H.; Hu, M.C.T.; Hemler, M.E.; Takada, Y.; Holzmann, B.; Weissman, I.L.  N,Aithler. Cloning and expression of cDNas for the alpha subunit of the murine lymphocyte  A;Reterence number: A41131; MJD:92066445; PMID:1846602  A;Reterence number: A41131; MJD:92066445; PMID:1846602  A;Reterence number: A41131  A;Reterence number: A41131 |
|---|--|--|
| Db 1092 VQLTAAABINTYNPBIYVIBDNTVIPLMIMKPDEKAEVPTGVIIGSIIA 1141 Qy 1101 GLILLALITAALYKLGFFKRQYKDM 1125  :    : | RESULT 11 A35854 Aiseasian alpha-1 chain precursor - rat (;Species: Rattus norregicus (Norway rat) C;Species: Rattus norregicus (Norway rat) C;Species: Rattus norregicus (Norway rat) C;Accession: A35894; Sil243 S;Ignatius, M.J; Large, T.H.; Houde, M.; Tawil, J.W.; Barton, A.; Esch, F.; Carbonetto, R.; Ignatius, M.J; Large, T.H.; Houde, M.; Tawil, J.W.; Barton, A.; Esch, F.; Carbonetto, J. Cell Biol. 111, 709-720, 139824 A;Accession: A35834 A;Accession: A3834 A;Accession | 167<br>167<br>167<br>167<br>167<br>167<br>167<br>167   |

| Db 212 YTKDLIVMGAPC   |  |                |
|---|--|----------------|
| Qy 343 ITSNGPLLSTV  | 1 -LPLIVGSSVGGLLLALITAALYKLGFFKRQYKDMMSE 1128  | δλ             |
| Db 204  | :  :     :       :  IBTSSLKFEIKATAFPEPHPKVIELNKDENVAHVFLEGLHHQRPKRHF   | qa             |
| QY 283 ELNTVASKPPRI   | DSVFTLLPGQGAFVRSQTETKVEPFEVPNP   | ٥x             |
| Db 161 -KNENKL  | :  | qa             |
| Qy 230 RKNAFKILFLL  | APVVNCSIAVCQRIQCDIPFFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEIL  | δλ             |
| Db 157 iFYI   | NSFLPQDDKLFNVLDVQTTTGQCHFKHYGRECTFAQQKGIAGTLTDIVKFLSKTD  | qq             |
| QY 170 LFSLMQYSEEF  | VRL  | ζ              |
| Db 134 -GVTLSRQPGE  | XYEVMLTVHGLVNPTSFVYGSSEBNEPETCMAEKINLTFHVINTGISMAPNVSVKIM  | QΩ             |
| Qy 110 FGSNLRQQPQK  | 906 VKYAVYMVYTSHGVSTKYLNFTASENTSRVMQHQYQVSNLGQRSLP-1SLVFL 957  | δλ             |
| Db 100 GKNPGQTCEQI  | : :     : :     : :     : : :     : : :     : : :     : : :     : : : :   :   : : : :   :   : : : :   :   : : : :   :   : : : : : : : : :   :  | qα             |
| Qy 53 STGSCEPI  | 848 SCSINHPIFPENSEVTFNITPDVDSKASLGNKLLLKANVTSENNMPRTNKTEFOLELP 905   | ò              |
| Db 40 YNVDTESALLY   |  | Ωp             |
| QY 1 FNLDTENAMTE  | VIVRNDGED  | δλ             |
| Xuely march<br>Best Local Similarity<br>Matches 293; Conserva | 735 PVLAEDAQR-LFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVGGPREFNV 787<br>   | cy<br>Cy       |
| F;40-1038/Product: integr                                     | 548 SDVITGSIRVSSSGEKCRTHQAFMRKDVRDILTPIHVEATYHLGHHVITKRNTEEFPPLQ 607   | qa             |
| C; Keywords: cell adhesion F:1-39/Domain: signal sec          | NSTRROTOVLGLTQTCETLKLQLPNCIEDP   | δλ             |
| A; Map position: 2q31-2q3                                     | 495ENGLPSVCMHLTLCFSYKGKEVPGYIVLFYNVSLDVHRKAESPSRFYFFSNGT 547   | qa             |
| A;Gene: GDB:ITGA4; CD49D                                      | QVVKGKEAGEVRVC   | λõ             |
| A; Residues: 40-50, 'E', 52-<br>C; Genetics:                  | 436 MFGQSISGQIDADNNGYUDVAVGAFQSDSAVLLRTRPVVIVEASLS-HPESVNRTKFDCT 494   | qa             |
| A; Accession: D28018  | 567 YFGQSLSGGQDLTMDGLVDLTVCAQGHVLLLRSQPVLRVKAIMBFNPREVARNVFECN 624   | à              |
| A; Title: The very late a:<br>A; Reference number: A941       | 377 ESIANLGDIDNDGFEDIALGAPQEDDIRGAVIYNGRV-DGISSTYSQRIEGQQISKSIR 435  | qa             |
| R, Takada, Y.; Strominger, Proc. Natl. Acad. Sci. U           | 507 AALTVLGDVNGDKLTDVAIGAPGEBDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQ 566   | λõ             |
| A; Cross-references: GB:M                                     | 320 VDLNADGFSDL-LVGAPMQSTIREEGRVFVY-INSGMGAVMVEMERVLVGSDKYA-ARFG 376   | gr             |
| A, Molecule type: DNA   | 448 VDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPLPRGQRA-RWQCDAVLYGEQGQPWGRFG 506   | Šī i           |
| A; Reference number: A393                                     | 20% AGAFKSFHIIEVVGGAPQHEQIGKAYIFSIDENELNIVYEMKGKKLGSYFGASVCA 319   | 3 (            |
| Proc. Natl. Acad. Sci. U                                      | ATTERNKVÇSLVLGAPKYQHIGLVAMFRQN   | ž f            |
| A; Cross-references: UNIP                                     | 202 NATITEMENTALES COLLINGIAN VINITAMENT - KUNUVARGSILGISVG 263  | è              |
| A; MOLECULE TYPE: MRNA A; Residues: 1-1038 <tak></tak>        | AGISSFYTODI I VAGA PIGS SYMPOTHETIVAL TAMENA VAN BENTA | du             |
| A) Accession: S06046  | PEGFSAAITSNGPLLSTVGSYDWAGGVFLYTSKEKSTFINMTRVDSDMNDAYFGYA   | δ              |
| A; Title: The primary str                                     | 203 ASC 205  | <del>Q</del> C |
| R, Takada, Y.; Elices, M.<br>EMBO J. 8, 1361-1368, 19         | 276 RSEKSRQELNTVASKPPRDHVFQANNFEALKTVQNQLREKIFAIEGTQTGSSSSFEHEMS 335   | δ              |
| C;Date: 01-Dec-1989 #sec<br>C;Accession: S06046: 239          | 191YTRKFGENF 202   | qu             |
| N;Alternate names: CD49d<br>C;Species: Homo sapiens           | 216 RKVVRELFNITNGARKNAFKILFILIDGEKFGDPLGYEDVIPELDREGVIRYVLGFGDAF 275   | δλ             |
| S06046<br>integrin alpha-4 chain r                            | 190 C 190  | අුය            |
| RESULT 13   | 156 LVSTIMBQLKKSKTLFSLMQYSEEFRIHFTFKEFQNNPNPRSLIKPITQLLGRTHTATGL 215   | Š              |
| Db 984 TIIITISLL  | 161 MKSDNKLPTGICYVMPSDLRTELSK  | qa             |
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Tr, J.L.; Hemler, M.E.
U.S.A. 84, 3239-3243, 1987
antigen family of heterodimers is part of a superfamily of molecu
ilS1; MUID:87204112; PMID:3033641
                                                                                                                                                                                                                                of VLA-4: homology to other inte
                                                                                                                                                                                                                                                                                                             K.S. L. L. L. L. BE.X16983; EMBL.X15356; NID:g33945; PIDN:CAA34852.1 eler, T.M.; Dean, D.C. U.S.A. 88, 4094-4098, 1991 ion of the alpha-4 integrin gene promoter.
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on; cytoskeleton; duplication; glycoprotein; heterodimer; transme
equence #status predicted <SIG>
grin VLA-4 alpha-4 chain #status predicted <MAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----NGEP----CG----KTCLEERDNQWL--- 133
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                                                                                             precursor - human
d; very late antigen-4 alpha chain; VLA-4 alpha chain
; (man)
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                                                                                                                                           FRQ-ENARGFGOSUV-QLQGSR--VVVGAPQEIVAAN----QRGSLYQCDY
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LLGLIVLLISCVMWKAGFFKRQYKSILQE 1022
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A;Accession: I58409
A;Accession: I58409
A;Accession: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1035 < RES>
A;Cross-references: UNIPROT:Q13797; GB:D25303; NID:g464180; PIDN:BAA04984.1; PID:g533327
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C;Species: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Dates: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: 158409; A49459
R;Hibi, K.; Yamakawa, K.; Ueda, R.; Horio, Y.; Murata, Y.; Tamari, M.; Uchida, Oncogene 9, 611-619, 1994
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                                                                                                                                                   SGGQDLTMDGLVDLTVGA--QGHVLLLRSQPVLRVKAIMEFNPREVARNVFECNDQVVKG
                                                                                                                                                                                                    631 KEAGEVRVCLHVQKSTRDRLREGQIQSVVTYDLALDSGR-----PHSRAVFNETKNSTRR
                                                                                                                                                                                                                   NRVQSLVLGAPRYQHIGLVAMFRQNTGMWESNANV----KGTQIGAYFGASLCSVDVDSN
               GSTDLVLIGAPHYYEQTRGGQVSVCPLPRGQRARWQC-DAVLYGEQGQPWGRFGAALTVL
                                                                         GFSDL-LVGAPMOSTIREEGRVFVY-INSGSGAVMNAMETNLVGSDKYA-ARFGESIVNL
                                                                                                 GDVNGDKLTDVAIGAPGEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGQSL
                                                                                                                  1020 PFFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAE----ILFN-
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      R;Palmer, E.L.; Ruegg, C.; Ferrando, R.; Pytela, R.; Sheppard, D.
J. Cell Biol. 123, 1289-1297, 1993
A;Title: Sequence and tissue distribution of the integrin alpha9 subunit,
A;Reference number: A49459; MUID:94064789; PMID:8245132
A;Accession: A49459
A;Accession: A4
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Ġ.
C.; Ferrando, R.; Pytela, R.; Sheppard,
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                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
10.7%; Score 630; DB 2; L. Best Local Similarity 26.5%; Pred. No. 1.8e-35; Matches 237; Conservative 160; Mismatches 332;
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| CV 1085FEVUREPIDLINGSSVGGLILANITANIXIGEPROGREMORY.111015  BESULT 18  RESULT 18 | Oy 923 YL<br>  Db 776 YVVPPFI              | Oy 961 RINQTVJ 1   |  |
|--|--|--|--|
|  | FEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMM | RESULT 15 T31437 integrin alpha chain SU2 - sea urchin (Lytechinus variegatus) integrin alpha chain SU2 - sea urchin (Lytechinus variegatus) C; Species: Lytechinus variegatus (variegated urchin) C; Species: Lytechinus variegatus (variegated urchin) C; Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004 C; Accession: T31437 A; Metzerote Data Library, May 1998 A; Pescription: Alpha SU2, a sea urchin integrin which binds laminin. A; Accession: T31437 A; Reference number: 221035 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Status: preliminary; translated from GB/EMBL, DDBJ A; Status: preliminary; translated from GB/EMBL, DDBJ A; Status: preliminary; translated from GB/EMBL, DDBJ A; Experimental source: developmental stage embryo C; Function: A; DBScxiption: binds laminin C; Superfamily: integrin alpha-2b chain | 10.5%; Score 614.5; DB 2; Length 1041; 5; Conservative 24.8%; Pred. No. 2.2e-34; 6; Conservative 155; Mismatches 314; Indels 245; Gaps OEGFSAITSNGP-LLSTVGSYDWAGGVFLYTSKEKSTFINMTRODSDMNDAYLG AGFGGIIFSDNSALWMGAPGSYLGGGIVVQSLLNRSV-VQATQESNTGTYSFDNSYRG YAAAI-ILKNRVQSLVLGAPRYQHI-GLVAMFRQNTGMWESNANVKGTQIGAYFGASLC 4  YSTALGDFNGDGVDDVVGTPRAESLMGLVAIFDONLNOPNOWGTQIVAYFGYSYT 2  SVDVDSNGSTDLVLIGAPHYYEOTRGGQVSVCPLPRGQBARWQCDAULYGGO VVDI-NNDTYDDLLVGAPMYMDDGPAIQ |

earch completed: November 9, 2004, 12:19:22 ob time : 34.25 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

November 9, 2004, 11:46:42; Search time 136.75 Seconds (without alignments) 4783.919 Million cell updates/sec Run on:

US-09-902-481B-3 5879

1 FNLDTENAMTFQENARGFGQ......FKRQYKDMMSEGGPPGAEPQ 1137 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1825181 segs, 575374646 residues Searched:

Total number of hits satisfying chosen parameters:

1825181

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt\_02:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description           | 1          |            |         | rac    |            | Tomorio .  | Officed and sapien | Badoloo min musculu | Obarha min muscu |          | י א ר<br>י | SOO .  | Veryba bos taurus | οα ς,      | F20701 homo sapien | mus     |        | O,    | l cypri | Η.       | o cypir | 5      | J ratt     | mus m      | <u> </u> | 1 rattu     | omou 6      | 5 homo     | sog o      |        | 7        | Aah65139 mus muscu |
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| SUMMARIES | ID                    | ITAM HIMAN | ITAM MOUSE | 09,1130 | 028984 | ITAX HUMAN | TTAD HIMAN | 06KAS4             | BAD21383            | ITAX MOUSE       | ITAD_RAT | ITAL_BOVIN | OFTVER | AA090015          | TTAL HIMAN | TTAL MOTTOR        | Ogwwy7a | 000000 | O9877 | O96481  | Contract | OBHZVO  | 088340 | TTAT WOTER | TTAE HIMAN | 088341   | TTA1 CITMON | TTAL DOMAIN | TTA2 HOWEN | TAND WOTEN | 060177 | 33466130 | Астерит            |
|           | DB                    |            | М          | 7       | N      | -          | H          | 8                  | N                   | Н                | П        | -          | N      | 2                 | , ,        |                    | ۱ ۸     | 1 0    | 10    | 10      | , (      | ۰ د     | ۱ ۸    | , -        | ٠,         | 10       | ٠.          | ٠.          | ٠,         | ٠,         | ٠,     | ۱ د      | 4                  |
|           | Query<br>Match Length | 1152       | 1153       | 1151    | 920    | 1163       | 1162       | 1188               | 1188                | 1169             | 1161     | 1165       | 1166   | 1166              | 1170       | 1163               | 1161    | 1160   | 1196  | 1086    | 1187     | 927     | 1167   | 1167       | 1179       | 1167     | 1151        | 1189        | 1170       | 1178       | 1178   | 1178     | 1                  |
| ₩ (       | Query                 | 99.1       | 75.6       | 74.1    | 64.4   | 58.8       | 57.6       | •                  |                     | 56.1             | 54.9     | 26.6       | 26.2   | 26.2              | 26.1       | 25.8               | 25.7    | 25.5   | 23.5  | 22.8    | 22.6     | 21.5    | 19.4   | 19.3       | 19.2       | 18.7     | 18.5        | 18.4        | 18.2       | 18.0       | 18.0   | 18.0     | ,<br>,<br>,        |
|           | Score                 | 5823.5     | 4          | 4358    | 3786.5 | 3456       | 3388       | 3306.5             | 3306.5              | 3297.5           | 3225.5   | 1561       | 1539   | 1539              | 1536.5     | 1516.5             | 1512.5  | 1502   | 1382  | 1341.5  | 1329.5   | 1264    | 1142.5 | 1136.5     | 1128       | 1097     | 1085.5      | 1079.5      | 101        | 1057       | 1057   | 1057     |                    |
| 1         | No.                   | Н          | 2          | m       | 4      | S          | 9          | 7                  | æ                   | 6                | 10       | 111        | 12     | 13                | 14         | 15                 | 16      | 17     | 18    | 19      | 20       | 21      | 22     | 23         | 24         | 25       | 26          | 27          | 28         | 29         | 30     | 31       |                    |

|   | D17301 homo canion | D10614 xattus | Pidel4 Idens norv | U/55/8 nomo sapien | Ferez musculu | Q/rdc3 mus musculu | 042094 gailus gall | NINGERAL MASCALA | Cownra mus sp. itg | OSMKI4 TELIS SLIVE | Ogress nomo sapien | Cappag nalocynthia | Q63001 rattus norv | Ospass musculu | Aah57200 mus muscu |
|---|--------------------|---------------|-------------------|--------------------|---------------|--------------------|--------------------|------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----------------|--------------------|
|   | ITA2 HUMAN         | ITA1 RAT      | TAKE TAKE         | TTAH MOTTER        | 074003        | 042094             | OBBS01             | COUNTRO          | OBMKE4             | OBTESE             | 800080             | 063001             | 100000             | Corce          | AAH57200           |
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| , | 1181               | 1180          | 1167              | 1188               | 1188          | 1171               | 1038               | י<br>ט<br>ט      | 1160               | 348                | 1332               | 200                | 300                | r<br>0         | 304                |
| 1 | F. 7               | 17.8          | 17.7              | 17.7               | 17.7          | 17.6               | 17.3               | 16.9             | 16.8               | 14.7               | 14.2               | 13.3               | 13.0               |                | 13.0               |
|   | 1054               | 1049          | 1042.5            | 1038.5             | 1038.5        | 1034               | 1020               | 993              | 986.5              | 865                | 837                | 784                | 761.5              | 1 .            | 761.5              |
| ć | 2.5                | 33            | 34                | 35                 | 36            | 37                 | 38                 | 39               | 40                 | 41                 | 42                 | 43                 | 44                 |                | 4                  |

## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO118; INTEGRINA.
PRINTS; PRO1181; INTEGRONAIN.
SWART; SM00191; Int_alpha; 5.
SWART; SM00191; Int_alpha; 5.
SPART; SN00221; VWA; 1.
PROSITE; PS50242; INTEGRIN ALPHA; 1.
PROSITE; PS50234; VWFA; 1.
PROSITE; PS50234; VWFA; 1.
TROSPORTED: Calcium; Cell adhesion; Direct protein sequencing; Glycoprotein; Integrin; Magnesium; Receptor; Repeat; Signal; Iransmembrane.
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Pfam; PF00357; Integrin_alpha; 1.
Pfam; PF00092; VWA; 1.
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PDB; IBHO; X-ray; 1/2=-
PDB; IIDN; X-ray; 1/2=-
PDB; IIDN; X-ray; 0=140-331.
PDB; IJIM; X-ray; 0=140-331.
PDB; IMIU; X-ray; 0=137-331.
PDB; IMIU; X-ray; A=137-331.
PDB; IMF7; X-ray; A=144-337.
PDB; IMF7; X-ray; A=144-335.
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EMBL; M18044; AAA59491.1;
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MIM; 120980; -.
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EMBL; S52154; A
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S52191;
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  MEDLINE=9826734; PubMed=9560195;

Oxvig C., Springer T.A.;

Cxvig C., 
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DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins DOMAIN: The integrin I-domains do not undergo protease cleavage.

SIMILARITY: Belongs to the integrin alpha chain family.

SIMILARITY: Contains 7 FG-ABP repeats.

SIMILARITY: Contains 1 VWFA domain.

DATABASE: NAMM=PROW; NOTE=CD guide CD11b entry;

WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd11b.htm".
                                                                                                                                                                                                                                                                                                                                                                   SECURNCE OF 17-31.
MEDLINE=87076671; PubMed=3539202;
Pierce M.W., Remold-O'Donnell E., Todd R.F. III, Arnaout M.A.;
Pierce M.W., Requence of human leukocyte glycoprotein Mol: conservation across species and homology to platelet IIb/IIIa.";
Biochim. Blophys. Acta 874:368-371(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-96363671; PubMed-8747460;
Lee J.O., Bankston L.A., Arnaout M.A., Liddington R.C.;
"Two conformations of the integrin A-domain (I-domain): a pathway for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lee J.O., Rieu P., Arnaout M.A., Liddington R.; "Crystal structure of the A domain from the alpha subunit of integrin CR3 (CD11b/CD18).";
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KEDLINE=98362595; PubMed=9687375;

Baldwin E.T., Sarver R.W., Bryant G.L. Jr., Curry K.A.,
Fairbanks M.B., Finzel B.C., Garlick R.L., Heinrikson R.L.,
Horton N.C., Kelley L.L., Midner A.M., Moon J.B., Mott J.E.,
Mutchler V.T., Tomich C.S., Matenpaugh K.D., Wiley V.H.;
"Cation binding to the integrin CD11b I domain and activation model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-M subsociates with beta-2.
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: Predominantly expressed in monocytes and
                                                                                                    Shelley C.S., Arnaout M.A.; "The promoter of the CD11b gene directs myeloid-specific and developmentally regulated expression.";
                                                                                                                                                                                                                                                   MEDLINE=9214986; PubMed=1346576;
Pahl H.L., Rosmarin A.G., Tenen D.G.;
"Characterization of the myeloid-specific CD11b promoter.";
                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 88:10525-10529(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 148-334.
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MEDLINE-95171458; PubMed-7867070;
       Proc. Natl. Acad. Sci. U.S.A. 86:257-261(1989).
                                                          SEQUENCE OF 1-9 FROM N.A.
MEDLINE=92073318; Pubmed=1683702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Structure 3:1333-1340(1995).
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                                                                                                                                                                                                                SEQUENCE OF 1-9 FROM N.A.
                                                                                                                                                                                                                                                                                                                             Blood 79:865-870(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell 80:631-638(1995).
                                                                                                                                              developmentally
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       activation?"
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| Db   976 RLNQTVIMDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDIP 1035   1021 FFGIQEFRATLKGNLSFDWYIKTSHNHLLIVSTAELLENDSVFTLLPGQGAFVRSQTET 1080  | SUL AM  | RN [1] RX MEDLINE=88312584; PubMed=3044779; RX MEDLINE=88312584; PubMed=3044779; RA Pytela R.; RT "Amino acid sequence of the murine Mac-1 alpha chain reveals homology with the integrin family and an additional domain related to von RT Willebrand factor."; RI EMBO J. 7:1371-1378(1988). RP SEQUENCE FROM N.A. (ISOFORM 2). RC STRAIN=C57BL/6J; TISSUE=Spinal cord; RX MEDLINE=2235463; PubMed=1256651; DOI=10,1038/nature01266; | RA Nikaido I., Osato N., Salto R., Ducuki H., Kondo S., RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., RA Balake J.A., Bradt D., Brusto V., Chothia C., Corbani L.E., Cousins S., RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., RA Gaasterland T., Garincich S., Hirokawa N., Jackson I.J., Jarvis E.D., RA Ganzerland S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D., RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., RA Maglott D.R., Maltais L., Manchionni L., McKenzie L., Miki H., RA Magashima T., Numata K., Okido T., Pavan W. J. Darres G. Doorle | RA Ravasi T., Reed J.C., Reed D.J., Raid B.Z., Ringwald M., R. Ravasi T., Reed J.C., Reed D.J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., RA Verardo R., Wangrer L., Wahlestedt C., Rang Y., Watanabe Y., Wells C., Wilming L.G., Wynshaw-Boris A., Yangisawa M., Yang L., Yang L., Yang L., Yang L., Yang L., Rhiraki C., Rawai J., Ziwmer A., Carninci P., Hayatsu N., Satok K., Rawai J., Aizawa M., Sakazume N., Sato K., Ra Hirozane-Kishikawa T., Komno H., Nakamura M., Sakazume N., Sato K., Ra Hirozane-Kishikawa T., Komno H., Nakamura M., Sakazume N., Sato K., Ra A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., RA Hara A., Hashizume W., Imotani K., Shinagawa A., Hashizume W., Imotani K., Shinagawa A., Hashizaki Y., Sasaki D., Shibata K., Shinagawa A., Hanalysis of the mouse transcriptome based on functional annotation of R. Malysis of the mouse transcriptome based on functional annotation of R. SeQUENCE OF 1150FE-591801.  R. BEQUENCE OF 11-45 FROM N.A.  R. SEGUENCE OF 11-45 FROM N.A.  R. Sastre L., Roman J.M., Teplow D.B., Dreyer W.J., Gee C.E., R. Larson R.S., Roberts T.M., Springer T.A.;  "A partial genomic DNA clone for the alpha subunit of the mouse |
|---|---|--|--|---|
| FT SIGNAL 1 16  FT CHAIN 17 1152 Integrin alpha-M.  Query Match  Query Match  99.1%; Score 5823.5; DB 1; Length 1152;  Best Local Similarity 98.8%; Pred. No. 0;  Matches 1123; Conservative 8; Mismatches 5; Indels 1; Gaps 1;  QY   FNLDTENAMTFOENARGFGGSVVQLQGSRVVVGAPQEIVAANQRGSLXQCDXTGSCEPI 60  DD 17 FNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLXQCDXSTGSCEPI 76 | 20POK<br>      <br> 20POK<br>      <br>      <br> |  |  | OY   661 YDLALDSGRPHSRAVFNETKNSTRROTGOVLGITOTCETLKLQLPNCIEDPVSPIVLRINF   720   721   1  |

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                                                                                                       MEDLINE=85188276; PubMed=3887182;

AM MEDLINE=85188276; PubMed=3887182;

AM MEDLINE=85188276; PubMed=3887182;

AM MEDLINE=85188276; PubMed=3887182;

AN Springer T.A., Teplow D.B., Dreyer M.J.;

The squence homology of the LEA-1 and Mac-1 leukocyte adhesion

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-!- SIMILARITY: Belongs to the integrin alpha chain family.
-!- SIMILARITY: Contains 7 FG-GAP repeats.
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Direct protein sequencing; Glycoprotein; Integrin; Receptor; Repeat;
complement receptor type 3 and cellular adhesion molecule Mac-1.";
Proc. Natl. Acad. Sci. U.S.A. 83:5644-5648(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=P05555-2; Sequence=VSP 010473;
Note=No experimental confirmation available;
-!- TISSUE SPECIFICITY: Predominantly expressed in monocytes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 obesity.
SUBUNIT: Heterodimer of an alpha and a beta chain. Alpha-M
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MGD; MGI:96607; Ltgam.

GO; GO:0008997; C:external side of plasma membrane; IDA.

GO; GO:0007155; P:cell adhesion; IMP.

GO; GO:0007155; P:cellular extravasation; IMP.

GO; GO:003593; P:neutrophil chemotaxis; IMP.

Interpro; PR000413; Integrin_alpha.

Interpro; IPR003235; VWFA.

Pfam; PF00357; Integrin_alpha; 1.

PRINTS; PR00185; INTEGRINA.

PRINTS; PR00185; INTEGRINA.

PRINTS; PR00453; VWFALOMAIN.

SMART; SM001927; VWA; 1.

SMART; SM001927; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         associates with beta-2.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- ALTERNATIVE PRODUCTS:
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IsoId=P05555-1; Sequence=Displayed;
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PROSITE; PS50234; VWFA; 1.
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EMBL; AK03944; BAC30350.1; -.
EMBL; M14293; AAA39484.1; -.
PIR; S00551; S00551.
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                                                                                                  SEQUENCE OF 17-28.
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     Integrin alpha-M.
Extracellular (Potential).
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75.6%; Score 4447; DB 1; :
Best Local Similarity 73.5%; Pred. No. 9.7e-287;
Matches 836; Conservative 147; Mismatches 153;
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                    HGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTWDGLVDLTVGAQGHVLLLRSQ
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                                                                                                                                         PRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLF
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Integrin beta 2 alpha subunit.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TAXID=10116;
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Fathallah D.M. Sr., Zerria K. Jr.;
Submitted (MAY-2010) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLUIAR LOCATION: Type I membrane protein (By similarity).
-!- SIMILARITY: Belongs to the integrin alpha chain family.
EMBL; AF268593; AAF81280.1; -.
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GO; GO:0008305; C:integrin complex; IEA.

GO; GO:0007160; P:cell-matrix adhesion; IEA.

GO; GO:0007229; P:integrin_mediated signaling pathway; IEA.

R InterPro; IPR000413; Integrin_alpha.

InterPro; IPR002035; VWF.A.

Pfam; PF001839; FG-GAP; 2.

R Pfam; PF000357; Integrin_alpha; 1.

R Pfam; PF00092; VWFA, 1.

R R PRINTS; PR01185; INTEGRINA.

R SMART; SM00191; Int alpha; 5.

R SMART; SM00191; Int alpha; 5.

R PROSITE; PS00242; INTEGRINA.

R PROSITE; PS00244; WWF, 1.
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VPVRLNQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQC 1017
                                                                                                           WAGGVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVA 417
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FLLTDGEKFGDPLGYEDVI PELDREGVIRYVLGFGDAFRSEKSRQELNTVASKPPRDHVF
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(Leu M5).
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Catarrhini; Hominidae; Homo.
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P20702; QBIVA6;
01-FEB-1991 (Rel. 17, Created)
01-CT-2004 (Rel. 45, Last sequence update)
01-CT-2004 (Rel. 45, Last annotation update)
Integrin alpha-X precursor (Leukocyte adhesion glycoprotein alpha chain) (Leukocyte adhesion receptor pi50,95) (CDILC) (Homo sapiens, Synonyms-CDILC)
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Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
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SEQUENCE FROM
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Lee J.-K., Schook L.B., Rutherford M.S.;

Louditted (NOV-1995) to the EMBL/GenBank/DDBJ databases.

Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.

-!- SUBCELLUIAR LOCATION: Type I membrane protein (By similarity).

-!- SIMILARITY: Belongs to the integrin alpha chain family.

EMBL; U40072; AAB16689.1;

GO; GO:00003105; C:integrin complex; IEA.

GO; GO:000160; P:cell-matrix adhesion; IEA.

InterPro; IPR000413; Integrin_alpha.

Refam; PF01839; FG-GAF; 3.

Pfam; PF01839; FG-GAF; 3.

PRINTS; PR01185; INTEGRINA.

REPRINTS; PR01185; INTEGRINA.

REPRINTS; PR01919; Int alpha; 4.
                                                                                                                     QLELPVKYAVYMVVTSHGVSTKYLNFTASENTSRVMQHQYQVSNLGQRSLPISLVFLVPV
                                                                                                                                   Gaps
          SGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRINKTEF
                                                                                 Euteleostomi;
Sus.
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Cetartiodactyla, Suina, Suidae,
                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
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Cell adhesion; Integrin; Transmembrane.
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Bukaryota; Metazoa; C.
Mammalia; Eutheria; C.
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SEQUENCE FROM N.A.
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01-FEB-1997 (
01-JUN-2003 (
CD11b (Fragme
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MEDLINE=223885; PubMed=12477932; DOI=10.1073/pnas.242603899;
A Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausberg R.L., Schemen C.M., Schuler G.D.,
A Lischul S.F., Ceeberg B., Buetow K.H., Scheafer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hisieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
B Capleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
B Bosak S.A., McEwan P.J., McKernan K.J., Make J.J., Hulyk S.W.,
A Raha S.S., Loquellano N.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Haley J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Shalska U., Smailus D.E.,
B. Chnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                         Corbi A.L., García-Aguilar J., Springer T.A.; "Genomic structure of an integrin alpha subunit, the leukocyte p150,95 molecule.";
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SIMILARITY: Belongs to the integrin alpha chain family.
SIMILARITY: Contains 7 FGAP repeats.
SIMILARITY: Contains 1 VWFA domain.
DATABASE: NAME=PROW; NOTE=CD guide CD11c entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd11c.htm".
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                                    Corbi A.L., Miller L.J., O'Connor K., Larson R.S., Springer T.A., "CDNA cloning and complete primary structure of the alpha subunit of Laukocyte adhesion glycoprotein, p150,95.";
EMBO J. 6:4023-4028(1987)
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MEDLINE=87167596; PubMed=3549901;
Miller L.J., Wiebe M., Springer T.A.;
Miller L.J., Wiebe M., Springer T.A.;
Purification and alpha subunit N-terminal sequences of human Mac-1 and p150,95 leukocyte adhesion proteins.";
J. Immunol. 138:2381-2383 (1987).
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SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: Predominantly expressed in monocytes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corbi A.L., Garcia-Aguilar J., Springer T.A.;
J. Biol. Chem. 265:12750-12751(1990).
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MEDLINE=88166645; PubMed=3327687;
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EMBL; M81695; AAA59180.1; -.

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PROSITE; PS00242; INTEGRIN ALPHA; 1.
PROSITE; PS50234; VWFA; 1.
3D-structure; Calcium; Cell adhesion; Direct protein sequencing;
Glycoprotein; Integrin; Magnesium; Polymorphism; Receptor; Repeat;
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W -> R (in dbSNP:11574633).
/FTId=VAR 01867?
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Extracellular (Potential)
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FG-GAP 4.
FG-GAP 6.
FG-GAP 6.
FG-GAP 7.
FG-GAP
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MIN' 151516; -.

GO; GO:0008305; C:integrin complex; TAS.
GO; GO:0004872; F:receptor activity; TAS.
GO; GO:0007155; F:receptor activity; TAS.
GO; GO:0009887; F:recal adhesion; TAS.
InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; VWF.A.
Pfam; PF00357; Integrin_alpha; 1.
PRINTS; PR01185; INTEGRINA.
PRINTS; PR01185; INTEGRINA.
SWART; SW00191; Int_alpha; 5.
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         M29487; AAAS1620.1; ALT SEQ.

M29482; AAAS1620.1; JOINED.

M29483; AAAS1620.1; JOINED.

M29484; AAAS1620.1; JOINED.

M29485; AAAS1620.1; JOINED.

M29486; AAAS1620.1; JOINED.
                                                                    EMBL; M29485; AAA51620.1; JO
EMBL; M29486; AAA51620.1; JO
EMBL; BC038237; AAH38237.1;
                                                                                                                                 PDB; 1N3Y; X-ray; A=141-338.
Genew; HGNC:6152; ITGAX.
MIM; 151510; -.
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SIGNAL 1
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  PVLRVKAIMBENPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVT
                                                                                                                                   SLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVG
                                                                                                                                                                                                                              GPREFNVTVVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEV
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                                    YDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNF
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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TISSUE-Spleen;
MEDLINES-96111956; PubMed=8777714;
Van der Vieren M., Le Trong H., Wood C.L., Moore P.F.,
Staunton D.E., Gallatin W.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
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Lrsor (Leukointegrin alpha
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Noti J.D., Johnson A.K., Dillon J.D.;
"Structural and functional characterization depen Child. Essential role of Sp1 and Sp3.";
J. Biol. Chem. 275:8959-8969(2000).
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"A novel leukointegrin; alpha d beta 2,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: Expressed moderately on myelomonocytic cell
lines and subsets of peripheral blood leukocytes and strongly on
atherosclerolized cells, including macrophages from cells within
atherosclerotic plaques, and on splenic red pulp macrophages.
DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins
with I-domains do not undergo protease cleavage.
SIMILARITY: Belongs to the integrin alpha chain family.
SIMILARITY: Contains 7 FG-GAP repeats.
SIMILARITY: Contains 1 VWFA domain.
                                                  MEDLINE=99059842; PubMed=9841932; Grayson M.H., Van der Vieren M., Sterbinsky S.A., Michael Gallatin W., Hoffman P.A., Staunton D.E., Bochner B.S.; "alphadbeta2 integrin is expressed on human eosinophils and functions as an alternative ligand for vascular cell adhesion molecule I (VCAM-
                                                                                                                                                                                                          INTERACTION WITH VCAMI.

MEDLINE=99370002; PubMed=10438935;
Van der Vieren M., Crowe D.T., Hoekstra D., Vazeux R., Hoffman P.A.,
Van der Vieren M., Crowe D.T., Hoekstra D., Vazeux R., Hoffman P.A.,
Grayson M.H., Bochner B.S., Gallatin W.M., Staunton D.E.;
"The leukocyte integrin alpha D beta 2 binds VCAM-1: evidence for a
binding interface between I domain and VCAM-1.";
J. Immunol. 163:1984-1990 [1999].
-!- FONGTION: Integrin alpha-D/Deta-2 is a receptor for ICAM3 and
VCAM1. May play a role in the atherosclerotic process such as
clearing lipoproteins from plaques and in phagocytosis of blood-
borne pathogens, particulate matter, and senescent erythrocytes
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PRINTS; PRO0185; VWFADOMAIN.
SWART; SMO0191; Int alpha; 5.
SWART; SMO0191; Int alpha; 5.
PROSITE; PSO0242; VWFA; 1.
PROSITE; PSO0243; VWFA; 1.
Calcium, Call adhesion; Glycoprotein; Integrin; Magnesium; Receptor; Signal; Transmembrana.
In Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0008305; C:integrin complex; TAS.
GO; GO:001537; P:cell-cell adhesion; NAS.
GO; GO:0007160; P:cell-matrix adhesion; NAS.
GO; GO:0006955; P:immune response; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000413; Integrin_alpha, InterPro; IPR002035; VWF A. Pfan, PF01839; FG-GAP; 3. Pfan; PF00035; VWA; 1.
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                                                                                                                                                                           Exp. Med. 188:2187-2191(1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 associates with beta-2.
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Gene 171:291-294(1996)
                                   INTERACTION WITH VCAM1
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61 RLOVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLRQQPQK 120
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          Extracellular (Potential).
Potential.
Cytoplasmic (Potential).
PG-GAP 1.
VWFA.
FG-GAP 3.
FG-GAP 4.
FG-GAP 5.
FG-GAP 5.
FG-GAP 6.
FG-GAP 7.
Potential.
Pote
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Matches 665; Conservative 168; Mismatches 288; Indels
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Integrin alpha-D
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IPR002035; VWF
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                                                                                                                                                                                                                                                                                                                                                                                                                                               VRLNQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDI
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                                                                                                                             PVLRVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVT
                                                                                                                                                                                                           HGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTVGAQGHVLLLRSQ
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                          PRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLF
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-!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
-!- SIMILARITY: Belongs to the integrin alpha chain family.
-!- AK131133; BAD21383.1; -.
GO, GO:0009897; C:external side of plasma membrane; IDA.
InterPro; IPR000413; Integrin_alpha.
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Sciurognathi, Muridae; Murinae; Mus
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Last sequence update)
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Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Rodentia,
NCBI_TaxID=10090;
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06KAS4

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                                                                                                                                                                                                                         56.2%; Score 3306.5; DB 2; Length 1188; 56.4%; Pred. No. 8.6e-211;
                                                                                                                                                                                          B8D93107BDBB4178 CRC64;
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Pfam; PF01839; FG-GAP; 3.
Pfam; PF01839; FG-GAP; 3.
Pfam; PF000357; Integrin_alpha; 1.
PRINTS; PF00195; VWA; 1.
PRINTS; PR00185; VWFADOMAIN.
SMART; SM00191; Int alpha; 5.
SWART; SM002172; VWA, 1.
PROSITE; PS50242; VWFA; 1.
Cell adhesion; Integrin; Transmembrane.
NOW TER
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SEQÜENCE 1188 AA; 131248 MW; BBD93107BDB41
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56.2%; Scote 3306.5;
Best Local Similarity 56.4%; Pred. No. 8.6e
Best Local Similarity Conservative 172; Mismatches
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STANDARD;
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Name=Itgax;
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AC 090XH4;
DT 05-JUL-2004
DT 05-JUL-2004
DT 05-JUL-2004
DE alpha chain)
GN Name=Itgax;
OS Mus musculus
OC Mammalia; EN CON NCEL TAXIDE;
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RP SEQUENCE FRE
RC TISSUE=Dend:
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             LACESASSTEVSGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSE
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                                             NNMPRTNKTEFQLELPVKYAVYMVVTSHGVSTKYLNFTASE-NTSRVMQHQYQVSNLGQR
                                                                                                                                           IAVCORIQCDIPFFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLP
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01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
MFLJ00114 protein (Fragment).
Mus musculus (Mouse)

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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EMBL, AK131133, BAD21383.1; -.
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GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR
                                                                                                                                                                                                                        -GVGRRWHCGTTLHGEQGHPWGRFGAALTVLGDVNGDSLADVAIGAPGEEENRGAVYIF
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Murinae; Murinae; Murinae; Murinae; Murinae; Murinae; Murinae; Mus
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05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Integrin alpha-X precursor (Leukocyte adhesion alpha chain) (Leukocyte adhesion plb)
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                           PRINTS, PROLISS; INTEGRINA.
PRINTS, PROLISS; VWFADOMAIN.
SMART; SMO0191; Int alpha; 5.
SMART; SMO0197; VMA; 1.
PROSITE; PSO024; INTEGRIN ALPHA; 1.
PROSITE; PSO024; VWFA; 1.
Calcium, Cell adhesion; Glycoprotein; Integrin; Magnesium; Receptor; Stepeat; Signal; Transmembrane.
SIGNAL
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GO; GO:0009897; C:external side of plasma membrane; IDA.
InterPro; IPR000413; Integrin_alpha.
InterPro; IPR02035; WMP_A.
                                                                                                                                                                                                                                                                                                                                 Integrin alpha-X.
Extracellular (Potential)
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N-linked (GlCNAc...) (N-linked (GlCNAc...)
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FG-GAP 1.
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FG-GAP 6.
FG-GAP 7.
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Pfam; PF00357; Integrin_alpha; 1.
Pfam; PF00092; VWA; 1.
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                                                                                                                                   20 FNLDAEKLTHFHMDGAEFGHSVLQYDSSWVVVGAPKEIKATNQIGGLYKCGYHTGNCEPI
                                                                                                                                                                                            80 SLQVPPEAVNISLGLSLAAAINPSWLLACGPTVHHTCRENIYLTGLCFLLSSSFKQS-QN
                                                                                                                                                                                                                                              FPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKELVSTIMEQLKKSKTLFSLMQYSEEF
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                                                                                                  1 FNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSTGSCEPI
                                                                     Gaps
                                                                   19;
                                Length 1169;
1169 AA; 129150 MW; C616412033C219A6 CRC64;
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                    56.1%; Score 3297.5; DB 1; 56.2%; Pred. No. 3.3e-210; Mismatches 306;
                                                                   Conservative 174; Mismatches
                                                     Local Similarity
les 641; Conserv
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                                                                                                                                                                                                                                                                                                                                                          Cloning of rat alpha D, a novel beta 2 integrin.";

Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.

-- FUNCTION: Integrin alpha-D/beta-2 is a receptor for ICAM3 and VCAM1. May play a role in the atherosclerotic process such as clearing lipoproteins from plaques and in phagocytosis of bloodbare pathogans, particulate matter, and senescent erythrocytes from the blood (By similarity).

--- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-D associates with beta-2 (By similarity).

--- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-D companies in the process of similarity.

--- SUBUNIT: Heterodimer of an imparance protein (By similarity).

--- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-D companies in the process of similarity.

--- SUBUNIT: The integrin I-domain (insert) is a VWFA domain. Integrins with I-domains do not undergo protease cleavage.

--- SIMILARITY: Contains 1 VWFA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Enropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                       IAVCQRIQCDIPFFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLP
                                                           GOGAFVRSOTETKVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMMSE
                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00191; Int alpha; 5.
SMART; SM00327; VWA; 1.
PROSITE; BS00242; INTEGRIN_ALPHA; 1.
PROSITE; PS50234; VWFA; 1.
Calcium; Cell adhesion; Glycoprotein; Integrin; Magnesium; Receptor;
Repeat; Signal; Transmembrane.
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                                                                                                                                                                                                                                                                                                                      STRAIN=Sprague-Dawley; O'Brien M., Kilgannon P.D., Dietsch Gallatin W.M.;
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Extracellular (Potential)
Potential.
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                                                                                                                                                                          05-JUL-2004 (Rel. 44, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF021334; AAF21241.1; -.
HSSP; P11215; 1BHQ.
InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; VWF.A.
Pfam; PF001839; PG-GAP; 3.
Pfam; PF000957; Integrin_alpha; 1.
Pfam; PF00095; VMA; 1.
PRINTS; PR01185; INTEGRINA.
PRINTS; PR01185; VWFADOMAIN.
                                                                                                                                                                                                                   Integrin alpha-D precursor.
Name=Itgad;
                                                                                                                                                                                                                                              Rattus norvegicus (Rat)
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87
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54.9%; Score 3225.5;
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1045 1045 N-1
1161 AA; 126600 MW;
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Matches 645; Conservative 163;
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24 YNLDVRHVQNFSFPLAGRHFGYRVLQV-GNGVVVGAPSE-
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By sim
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GFFKR motif
SIMILARITY: Contains 7 FG-GAP repea
SIMILARITY: Contains 1 VWFA domain.
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FG-GAP 4.
FG-GAP 5.
FG-GAP 6.
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PROSITE; PS50234; VWFA; 1.
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HTAL BOVIN

STANDALL,

PG1625,

05-JUL-2004 (Rel. 44, Last sequence update)

05-JUL-2004 (Rel. 44, Last sequence update)

05-JUL-2004 (Rel. 44, Last annotation update)

11tegrin alpha-L precursor (Leukocyte adhesion glycoprotein LFA-1

Integrin alpha-L precursor (Leukocyte function associated molecule 1, alpha
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SUBUNIT: Hetrocimer of an alpha and a beta subunit. Alpha-L subccitlura Location: Type I membrane protein (By similarity).

SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins with I-domains do not undergo protease cleavage.

SIMILARITY: Belongs to the integrin alpha chain family.
                                          677 DLALDPGKLISRAIFDETKNCTLTGRKTLGLGDHCETVKLLLDDCVEDAVSPIILRINFS
                                                                                                                                                                                                                                                                                                                                                                                                                 913 LELPVKYTVYTLISRQEDSTNHVNFSSSHGGRRQEAAHRYRVNNLSPLKLAVRVNFWVPV
                                                                                                                                                                 LVGTPLSAFGNLRPVLAEDAORLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVGG
                                                                                                                                                                                        782 PREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEVS
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                                                                                                                                                                                                                                                                                                                                                                                        LELPVKYAVYMVTSHGVSTKYLNFTASENTSR-VMQHQYQVSNLGQRSLPISLVFLVPV
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                   VLRVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVTY
                                                                                            DLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus (Bovine).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
PubMed=14697514; DOI=10.1016/j.gene.2003.09.043;
Fett T., Zecchinon L., Baise E., Desmecht D.;
"The bovine (Bos taurus) CD11a-encoding cDNA: molecular cloning, characterisation and comparison with the human and murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TKVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMM 1126
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Gene 325:97-101(2004).
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                                                                                                                                                                                                                                                                                      Integrin alpha-L.
Extracellular (Potential)
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Conservative 200; Mismatches 468;
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PROSITE; PS00242; INTEGRIN_ALPHA; 1.
PROSITE; PS50234; WWFA; 1.
Call adhesion; Integrin; Transmembrane.
SEQUENCE 1166 AA; 128723 WW; 7BBDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative 199;
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PRINTS; PROGAS3; VWFADOMAIN.
SMART; SMO0191; ILL_alpha; 5.
SMART; SMO0327; VWA; 1.
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                                                                               NCBI_TaxID=9913;
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LLTDGEKFGDPLGYEDVI PELD-REGVIRYVLGFGDAFRSEKSRQELNTVASKPPRDHVF
                         :| : :||| : :|| | : :|| : | : :|| : | : :|| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
                                                                                                    OVSVCPLPRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDN
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                                                                           QANNFEALKTVQNQLREKIFAIEGTQTGSSSSFEHEMSQEGFSAAITSNGPLLSTVGSYD
                                                                                                                                                  WAGGVF-LYTSKEKSTFINMTRVDSDMNDAYLGYAAA-IILRNRVQSLVLGAPRYQHIGL
                                                                                                                                                                                      WAGGFLDLKADLKSSTFVGNEPLTVESRAGYLGYTVTWLPSRGTMSLLATGAPRYQHVGR
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Lymphocyte function-associated antigen 1 alpha subunit CD11a.
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298 258 416 474 371 :|:| LLFQQPKRGGPWSQIQEIDGIQIGSYFGGELCGVDVDRDGETELLLIAAPLYYGEQRGGR 491 661 80 651 28 GAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTVGAQGHV 594 139 LOGHPGYQECIKGNVDLVFLFDGSMSLQQDEFEKIVDFMKDVMKKLSNSSYQFAAVQFST 199 YFRTEFTFLDYIKQKDPDALLAGVKHMRLLTNTFGAINYVAKEVFRPDLGARPDATKVLI 119 QKFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKELVSTIMEQLKKSKTLFSLMQYSE **EPRIHFTFKEFQNNPNPRSLIKPITQLLGRTHTATGLRKVVRELFNITNGARKNAFKILF** LLTDGEKFGDPLGYEDVIPELDREGVIRYVLGFGDAFRSEKSRQELNTVASKPPRDHVFQ 299 ANNFEALKTVONOLREKIFALEGTOTGSSSSFEHEMSQEGFSAALTSNGPLLSTVGSYDW 1 FNLDTENAMTFQENARG--FGQSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSTGSCE PIRLQVPVBAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLRQQP AMFRQ--NTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQ AGGVF-LYTSKEKSTFINMTRVDSDMNDAYLGYAAA-IILRNRVQSLVLGAPRYQHIGLV VSVCPLPRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNR LLLRSQPVLRVKAIMEFNPREVARNVFECNDQVVKGKEAG-EVRVCLHVQK--STRDRLR Dileepan T., Thumbikat P., Kannan M.S., Maheswaran S.K.; Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
-!- SIMILARITY: Belongs to the integrin alpha chain family.
Bell; AX38258; AAQ90015.1; -.
InterPro: IPR002035; VWP.A.
InterPro: IPR002035; VWP.A.
Pfam; PF00383; Integrin\_alpha; 1.
Pfam; PF00395; Integrin\_alpha; 1. Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae, Bovinae, Bos 7BBD8AFBA896C9DF CRC64; 5; 9; DB 2 4e-93; Score 1539; DB Pred. No. 4e-93 9; Mismatches

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139 LQGHPGYQECIKGNVDLVFLFDGSMSLQQDEFEKIVDFMKDVMKKLSNSSYQFAAVQFST
                                                                                                 LL TDGEKFGDPLGYEDVI PELDREGVI RYVLGFGDAFRSEKSRQELNTVASKPPRDHVFQ
                                                                                                                     606 IVLSSRPWVDIITSVSFSPAEIPVHEVECSYSTSNQKKEGVNLTVCFQVKSLIST---F
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                                EPRIHFTFKEFQNNPNPRSLIKPITQLLGRTHTATGLRKVVRELFNITNGARKNAFKILF
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                      EGQIQSVVTYDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPV
                                                                                       SPIVLRINFSL --- VGTPLS -- AFGNIRPVLAEDAQRIFTALFPFEKNCGNDNICQDDLS
                                                                                                                                                                                   LAFSDMRSKILRLTPSASLSVRLTLRNTAEDAYWVQVTLSFPQGLSFRKVEIL---KPHS
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Lymphocyte function-associated antigen 1 alpha subunit CD11a.
Bos taurus (Bovine).
Bulkaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
NGB TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26.2%; Score 1539; DB 2; Length 1166; llarity 34.3%; Pred. No. 4e-93; Conservative 199; Mismatches 472; Indels 106;
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Dileepan T., Thumbikat P., Kannan M.S., Maheswaran S.K.,
"Molecular cloning and sequencing of bovine CD11a.";
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AY382558; AAQ90015.1; -
SEQUENCE 1166 AA; 128723 MW; 7B8DBAFBA896C9DF CRC64;
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GO; GO:0008305; C:integrin complex; GO; GO:0006528; P:cell motility; TAL InterPro; IPR000413; Integrin_alpha. InterPro; IPR002035; WWF A.
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PROSITE; PS50234; VWFA; 1.
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Pfam; PF00357; Integrin_alpha; 1.
Pfam; PF00092; VWA; 1.
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1MQ9; X-ray; A=152-330.

11ZON; X-ray; A=150-336.

11ZOO; X-ray; Q=150-336.

11ZOO; X-ray; A/B=150-336.
                                                                                                                                                                                                                                                                             1CQP; X-ray; A/B=153-334.
1DGQ; NMR; A=149-336.
1LFA; X-ray; A/B=-.
1MJN; X-ray; A=153-331.
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PRINTS; PR00453; VWFADOMAIN.
SMART; SM00191; Int_alpha; 5.
SWART; SM00327; VWA; 1.
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S03308; S03308.
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MIM; 15
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PDB;
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 P20701, 043746;
01-FEB-1991 (Rel. 17, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-CCT-2004 (Rel. 48. annotation update)
Integrin alpha-L precursor (Leukocyte adhesion glycoprotein LFA-1
alpha chain) (LFA-1A) (Leukocyte function associated molecule 1, alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qu.A., Leahy D.J.;
"Crystal structure of the I-domain from the CD11a/CD18 (LFA-1, alpha L beta 2) integrin.";
Proc. Natl. Acad. Sci. U.S.A. 92:10277-10281(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 153-334.
MEDLINE=99425288; PubMed=10493852;
Kallen J., Welzenbach K., Ramage P., Geyl D., Kriwacki R., Legge G., Cottens S., Weitz-Schmidt G., Hommel U.,
"Structural basis for LFA-1 inhibition upon lovastatin binding to the "Structural basis for LFA-1 inhibition upon lovastatin binding to the "Olla I-domain.",
J. Mol. Biol. 292:1-9(1999).
-!- FUNCTION: Integrin alpha-L/beta-2 is a receptor for ICAMI, ICAM2, Including leukocyte-endothelial cell interaction, cytocoxic T-cell mediated killing, and antibody dependent killing by granulocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins with I-domains do not undergo protease cleavage. SIMILARITY: Belongs to the integrin alpha chain family. SIMILARITY: Contains 7 FG-GAP repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qu A., Leahy D.J.;
"The xole of the divalent cation in the structure of the I domain from the CD11a/CD18 integrin.";
Structure 4:931-942(1996).
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 1), AND PARTIAL SEQUENCE.
MEDLINE=89139887; PubMed=253322;
Larson R.S., Corbi A.L., Bernan L., Springer T.;
"Primary structure of the leukocyte function-associated molecule-1
alpha subunit: an integrin with an embedded domain defining a protein superfamily.";
Cell Biol. 108:703-712(1989).
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 2).

MEDLINE=9945270; PubMed=10493829;
Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon R.,
Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L.,
Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S.,
Eichler E.E., Harris P.C., Venter J.C., Adams M.D.;
"Genome duplications and other features in 12 Mb of DNA sequence from human chromosome 16p and 16q";
Genomics 60:295-308(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 153-335, AND REVISION TO 214. MEDLINE=96036067; PubMed=7479767;
                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SUBCELLULAR LOCATION: Type I membrane protein.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Note=No experimental confirmation available; TISSUB SPECIFICITY: Leukocytes.
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PRT; 1170 AA
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IsoId=P20701-1; Sequence=Displayed;
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                                                                                                                           chain) (CD11a).
Name=ITGAL; Synonyms=CD11A;
STANDARD;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation — the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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3 IGNAL 1 25

CHAIN 26 1070 Extracellular (Potential).

TRANSMEM 1091 1111 POTENTIAL.

DOMAIN 1112 1111 POTENTIAL.

REPEAT 42 91 FG-GAP 1.
SIMILARITY: Contains 1 VWFA domain.
DATABASE: NAME=PROW; NOTE=CD guide CD11a entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd11a.htm".
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FG-GAP 1. 
FG-GAP 2. 
WWFA.
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FG-GAP 4.
FG-GAP 6.
FG-GAP 6.
FG-GAP 7.
FG-GAP 6.
FG-GAP
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                 DNICODDLSITESFMSLDCLVVGGPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVS
                                                                              GEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTV
                                                                                                                                           GAQCHVLLLRSQPVLRVKAIMEFNPREVARNVFECNDQVV-KGKEAGEVRVCLHVQKSTR
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IGLVAMFR--QNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQT
                                                            RGGQVSVCPLPRGQRARWQCDAV--LYGEQGPWGRFGAALTVLGDVNGDKLTDVAIGAP
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; Murinae; Mus
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MEDLINE-21268576 PubMed=2051027;

Kaufmann Y., Tseng E., Springer T.A.;

"Cloning of the murine lymphocyte function-associated molecule-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mans musculus (Mouse).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; B
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLALITAALYKLGFFKRQYKDMMSEG-GPPGAEP 1136
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01-MAR-1992 (Rel. 21, Last sequence update)
02-ULL-2004 (Rel. 44, Last annotation update)
Integrin alpha-L precursor (Leukocyte adhesion
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chain) (CD11a).
Name=Itgal; Synonyms=Lfa-1;
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P24063;
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    QQPQKFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKELVSTIMEQLKKSKTLFSLM

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                    leukocytes recruitment.
SUBNUT: Heterodimer of an alpha and a beta subunit. Alpha-L
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: Leukocytes.
DOWAIN: The integrin I-domain (insert) is a VWFA domain. Integrins with I-domains do not undergo protease cleavage.
SIMILARITY: Contains 7 FG-GAP repeats.
SIMILARITY: Contains 1 VWFA domain.
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Extracellular (Potential)
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its expression in COS cells.";
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GFFKR motif.
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FG-GAP 4.
FG-GAP 5.
FG-GAP 6.
FG-GAP 7.
Potential.
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PIR; I56126; I56126.
HSSP; P20701; 1DG0.
MGD; MG19.6606; Itgal.
InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; VWF_A.
                                                                         MEDLINE = 85188276; PubMed = 3887182;
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768 TFSFMSLDCLVVGGP-----REFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQN 821
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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9, 2004, 11:45:42; Search time 103.25 Seconds (without alignments) 3950.365 Million cell updates/sec November Run on:

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1 FNLDTENAMIFQENARGFGQ......FKRQYKDMMSEGGPPGAEPQ 1137

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Sequence:

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2002273 seqs, 358729299 residues Searched:

2002273 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:\*

## STIMMARTES

| Human Bet | Human bet | Human Bet | Human alp |          | Human alp | Human Bet | Rat alpha | Rat      | Rat      | Rat      | Rat alpha | Rat      | Rat beta- | Rat alpha | Mous     | Mouse alp | Mouse    | Mouse alp | Mouse    |
|-----------|-----------|-----------|-----------|----------|-----------|-----------|-----------|----------|----------|----------|-----------|----------|-----------|-----------|----------|-----------|----------|-----------|----------|
| Abq61468  | Aaw23064  | Aaw65106  | Aaw7283   | Aaw73343 | Aab07376  | Abg61485  | Aar78169  | Aaw23062 | Aaw60004 | Aaw72824 | Aab07374  | Abg61483 | Aaw65104  | Aaw73345  | Aaw23061 | Aaw60003  | Aaw65103 | Aaw72836  | Aaw73347 |
|           |           |           |           |          |           |           |           |          |          |          |           |          |           |           |          |           |          |           |          |
| ABG61468  | AAW23064  | AAW65106  | AAW72837  | AAW73343 | AAB07376  | ABG61485  | AAR78169  | AAW23062 | AAW60004 | AAW72824 | AAB07374  | ABG61483 | AAW65104  | AAW73345  | AAW23061 | AAW60003  | AAW65103 | AAW72836  | AAW73347 |
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| 57.6      | 57.4      | 57.4      | 57.4      | 57.4     | 57.4      | 57.4      | 54.7      | 54.7     | 54.7     | 54.7     | 54.7      | 54.7     | 54.5      | 54.5      | 54.4     | 54.4      | 54.4     | 54.4      | 54.4     |
| 3388      | 3372.5    | 3372.5    | 3372.5    | 3372.5   | 3372.5    | 3372.5    | 3215.5    | 3213.5   | 3213.5   | 3213.5   | 3213.5    | 3213.5   | 3206.5    | 3206.5    | 3201     | 3201      | 3201     | 3201      | 3201     |
| 56        | 27        | 28        | 59        | 30       | 31        | 32        | 33        | 34       | 35       | 36       | 37        | 38       | 39        | 40        | 41       | 42        | 43       | 44        | 45       |
|           |           |           |           |          |           |           |           |          |          |          |           |          |           |           |          |           |          |           |          |

## ALIGNMENTS

Beta-integrin alpha-d subunit; human; modulator; treatment; psoriasis; type-I diabetes; atherosclerosis; multiple sclerosis; asthma; lung inflammation; acute respiratory distress syndrome; CD11b subunit; rheumatoid arthritis. Human Beta-integrin CD11b subunit protein. AAW65090 standard; protein; 1153 AA. (first entry) sapiens 28-SEP-1998 US5728533-A. 17-MAR-1998 AAW65090; Homo AAW65090 

95US-00485618. 07-JUN-1995; 23-DEC-1993;

93US-00173497. 94US-00286889. 94US-00362652. (ICOS-) ICOS CORP. 05-AUG-1994; 21-DEC-1994;

Gallatin WM; Van Der Vieren M,

WPI; 1998-206565/18.

Screening assay for modulators of integrin binding - using immobilised or labelled alpha-d polypeptide, useful for, e.g. treating type-I diabetes.

Example 5; Fig 1A-D; 106pp; English.

This sequence represents a human beta-integrin CD11b subunit which is used to describe a method for identifying compounds that modulate the interaction of the beta-integrin alpha-d subunit with a binding partner of alpha-d which involves contacting an alpha-d polypeptide with an alpha-d binding partner, one of which is immobilised and the other of which is labelled, in the presence of a test compound, and determining if the compound affects binding between the alpha-d polypeptide and alpha-d binding partner, where the alpha-d polypeptide is alpha-d or its fragment comparising the cytoplasmic, transmembrane or extracellular domain of alpha-d. Compounds that modulate alpha-d binding could be used to treat

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as type-I diabetes, atherosclerosis, multiple sclerosis, asis, lung inflammation, acute respiratory distress syndrome
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                                                                                                                                             FNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSTGSCEPI
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                                                                                                                 8; Mismatches
                                                                                     Score 5839;
Pred. No. 0;
                                                                                                    Pred. No.
                                                                                     99.3%;
98.9%;
             asthma, psoriasis, lung i and rheumatoid arthritis
                                                                                                                 Matches 1124; Conservative
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                                                         Sequence 1153 AA;
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                                                                                                                                                                                                                   Human; macrophage infiltration inhibition; alpha d integrin; leukocyte integrin; Leu-CAM; leukointegrin; immune response; inflammation; leukocyte adhesion deficiency; LAD; Type I diabetes; atherosclerosis; multiple sclerosis; asthma; psoriasis; beta2 integrin; lung inflammation; acute respiratory distress syndrome; Crohn's disease; rheumatoid arthritis; central nervous system injury; CD11b.
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Example 5; Fig 1; 270pp; English.

Integring are a class of membrane-associated molecules that participate in cellular adhesion. Integrins are made up of an alpha subunit and a beta subunit. One class of human integrins are restricted to expression in white blood cells and have a common beta2 subunit: the leukocyte cintegrins, Leu-CAMS, leukointegrins or beta2 integrins. Beta2 integrins have an importent role in immune and inflammatory responses. The present protein sequence is the human integrin alpha subunit CD11b. This sequence was used in an alignment to identify a novel beta2 integrin alpha approximately 60% identity to the protein sequence of alpha d. The capproximately 60% identity to the protein sequence of alpha d. The capproximately 60% identity to the protein sequence of alpha d. The capproximately for diseases linked to aberrant alpha d function e.g. Type I diabetes, atherosclerosis, multiple classis, asthma, psoriasis, lung inflammation, acute respiratory distress syndrome, rheumatoid arthritis and leukocyte adhesion deficiency (LAD). In addition, anti-alpha d monoclonal antibodies may be used in the inhibition of macrophage infiltration at the site of a central nervous system injury. The monoclonal antibodies can also be used to detect and diagnose Crohn's disease

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                       Score 5839;
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This invention relates to a modified integrin-I or integrin I-like domain to polypeptide comprising at least one disulfide bond so that the domain is stabilised in a desired conformation. The polypeptide of the invention or may have antiinflammatory or imunosupressive activities. The many have antiinflammatory or imunosupressive activities. The solf-peptides of the invention have an open conformation and are useful as immunogens to produce autibodies that selectively bind to integrin I-c domain; and for identifying a modulator of integrin activity, or of for interaction of an integrin and a cognate ligand. The polypeptide of the invention, or antibodies (preferably anti-LFA-I antibody) is useful for treating or preventing an integrin mediated disorder which is a an integrin to a cognate ligand such as Crohn's disease.

Composition comprising the a cognate ligand such as Crohn's disease.

Composition comprising the peptide of the invention is useful for composition comprising the peptide of the invention is useful for treating an integrin mediated disorder in a subject. The polypeptides and/or active or antigent fragments are useful as reagents for diagnosis of integrin-I alpha-M protein subunit used to generate the mutant
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Human Beta2 integrin alphaCD11b subunit.
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Beta2 integrin, alphaD subunit, CD11c subunit, CD11b subunit, LAD; leukocyte adhesion deficiency; inflammatory response; diabetes; unulippe sclerosis, aneuroprotective; inflammatory bowel disease; Crohn's disease; ulcerative colitis; immune complex alveolitis; leukaemia; ICAM-R; VCAM-1; anti-inflammatory; infracellular cell adhesion molecule; vascular cell adhesion molecule; autonomic dysfunction; sensory dysfunction; spinal cord injury.

orUse of an anti-alpha-d monoclonal antibodies for promoting locomotor recovery, inhibiting locomotor damage, limiting locomotor impairment, or limiting autonomic and sensory dysfunction following spinal cord injury.

Example 5; Page 191-194; 270pp; English.

The invention relates to promoting locomotor recovery, inhibiting concounts damage, limiting locomotor impairment, or limiting autonomic locomotor damage, limiting locomotor impairment, or limiting autonomic and sensory dysfunction following spinal cord injury victim. The method also involves the use of a ligand cord injury victim. The method also involves the use of a ligand cord injury victim. The method is useful for promoting component cell adhesion molecule. The method is useful for promoting locomotor recovery, inhibiting locomotor damage, limiting locomotor impairment, or limiting autonomic and sensory dysfunction following spinal cord injury. In particular, the spinal cord injury comprises compression of the spinal cord. The antibodies are also useful for reducing inflammation at the site of a central nervous system injury. The specification also details the identification of Beta2 integrin alphab cord in raising the antibodies. Beta2 integrins of are implicated in diseases such as LAD (leukcoyte adhesion deficiency, inflammatory response, diabetes, multiple sclerosis, arthritis, graft collins, immune complex alveolitis and leukemia. The present sequence is a Beta2 integrin alphab protein sequence included for comparison with the beta2 integrin alphab protein sequences

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Pred. No. 0;
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The invention comprises structurally biased variant integrin inserted (I)

domain proteins, wherein the alterations to the protein occur in at least

two noncontinuous regions. Specifically the the variant integrin I domain

proteins are structurally biased to exist in the open conformation.

thereby altering the binding ability of the protein. The invention also

comprises nucleic acids encoding the variant integrin I domain proteins.

The integrin I domain proteins and nucleic acids are useful for treating,

preventing or suppressing integrin related inflammatory and immunological

disorders (e.g. rheumatoid arthritis). The variant integrin I domain

C proteins and nucleic acids can also be used for treating: ischaemia/

c reperfusion (e.g. hypovolemic shock); infarction, cerebral shock, viral

c infection; and cancer. The variant integrin I domain nucleic acids and

proteins may be used in gene therapy, as vaccines and to screen for

c bloactive agents. The present amino acid sequence represents the Mac-1
                       FFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLPGQGAFVRSQTET 1080
                                                                                                                                                                                                                                                                                                                      Mac-1; integrin alpha subunit; variant integrin inserted domain protein; open conformation; integrin related inflammatory disorder; integrin related immunological disorder; rheumatoid arthritis; ischaemia; reperfusion; hypovolemic shock; infarction; cerebral shock; viral infection; cancer; gene therapy; vaccine;
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Best Local Similarity 98.9%;
Matches 1124; Conservative
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The invention relates to a binding domain-immunoglobulin fusion protein comprising a binding domain polypeptide that is fused to an immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain CH2 constant region polypeptide that is fused to the hinge region polypeptide that is fused to the hinge region polypeptide that is fused to the CH2 constant region polypeptide comprises: a wild-type human IgG1 immunoglobulin hinge region polypeptide, a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues; where the mutated human IgG1 immunoglobulin hinge region polypeptide contains 2 cysteine residues, where the first cysteine is not mutated; a mutated human IgG1 immunoglobulin hinge region polypeptide contains 3 or more cysteine residues, where the mutated human IgG1 immunoglobulin hinge region polypeptide contains or cysteine residue; and a mutated human IgG1 immunoglobulin hinge region polypeptide contains or cysteine residue a mutated human IgG1 immunoglobulin hinge region polypeptide contains contains the mutated human IgG1 immunoglobulin hinge region polypeptide contains con cysteine residues the mutated human IgG1 immunoglobulin hinge region polypeptide contains con cysteine residues the mutated human IgG1 immunoglobulin hinge region polypeptide contains con cysteine residues the mitated human IgG1 immunoglobulin hinge region polypeptide contains con cysteine residues the mitated human IgG1 imminoglobulin hinge region polypeptide contains con cysteine residues the mitated human IgG1 imminoglobulin hinge region polypeptide contains con cysteine residues the mitated human IgG1 imminoglobulin hinge region protein is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New binding domain-immunoglobulin fusion protein, useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, Grave's disease or autoimmune disease.
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Binding domain; immunoglobulin; fusion protein; cytostatic; antiarthritic; immunosuppressive; antidiabetic; antithyroid; antiarthritic; immunosuppressive; antidiabetic; antithyroid; characterive; hinge region; fimmunoglobulin heavy chain; cH2 constant region; GH3 constant region; GH3 constant region; GH3 constant region; GH3 constant region; antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation; antigion; earliannoma; carcinoma; sarcoma; rheumatoid arthritis; myasthenia gravis; Grave's disease; type I diabetes mellitus; multiple sclerosis; autoimmune disease.
Binding domain-immunoglobulin fusion protein-associated protein #85
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17-JAN-2002; 2002US-00053530.
03-JUN-2002; 2002US-0385691P.
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pharmaceutical composition comprising the binding domain-immunoglobulin fusion protein or polymucleotide and a carrier, and treating a subject having or suspected of having a malignant condition or a B-cell disorder. The binding domain-immunoglobulin fusion protein is useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis, mysathenia gravis, Grave's disease, type I diabetes mellitus, multiple sclerosis or autoimmune disease. The present sequence is a binding domain-immunoglobulin fusion protein-associated protein sequence. Note: The immunoglobulin for this patent formed part of the printed specification and is also available in electronic formed trectly from USPTO at sequence that sequence that printed specification in dentified the sequences in the printed specification by their SEQ ID number therefore none of the sequences can be explicitly identified.
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Sequence 1153 AA;

| Similarity 98.9%; Score 5839; DB 7; Length 1153;<br>S4; Conservative 8; Mismatches 5; Indels 0; Gaps 0; |       | 7 FNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSTGSCEPI 76 |        | 7 RLQVPVEAVNMSLGISLAATISPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLRQQPQK 136 | PPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKELVSTIMEQLKKSKTLFSLMQYSE | 7 FPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEF 196 | RIHFTFKEFQNNFNPRSLIKPITQLLGRTHTATGLRKVVRELFNITNGARKNAFKILFLL 240 |      | TDGEKFGDPLGYEDVIPELDREGVIRYVLGFGDAFRSEKSRQELNTVASKPPRDHVFQAN 300 |      | NFBALKTVQNQLREKIFALEGTQTGSSSSFEHEMSQEGFSAALTSNGPLLSTVGSYDWAG 360 |         | GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR 420 |          | QNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYRQTRGGQVSVCPL 480 |       | PRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYL |      |         | HGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTVGAQGHVLLLRSQ 616 |      | 7 PVLRVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVT 676 | YDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNF 720 | YDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNC1EDPV6 | SLVGTPLSAFGNLREVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVG 780 |         |
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| ·   | 1 FNL | 17 FNL  | 61 RLC | 77 RLC   | .21 FPE  | 137 FPE  | 81   | 26   | 241 TDG  | 57   | 10   | 317 NFE | 61   | 377 GVF  | 421 QNT  | 37    | 81  | 97   | 541 HGT | 57   | 10   | 617 PVL  | 61   | 677 YDL  | 721 SLV  | 737 SLV |
| Query Match<br>Best Local S<br>Matches 1124   | δ     | qu  | ò      | qa   | Qy 1   | Db 1   | Qy 1   | Db 1 | Qy 2   | Db 2 | Oy 3   | Db 3:   | Qy 3   | 3.<br>Dp | Qy 4.  | Db 4. | Qy 4.   | Db 4 | Qy 5.   | Db 5   | οy 6 | 9 qa   | Qy 6   | 9 qa   | Qy 7   | Db 7.   |

| Qy         781 GPR           Db         797 GPR           Qy         841 SGA           Qy         841 SGA           Qy         901 QLB           Db         917 QLB           Qy         961 RLN           Qy         1021 FPG           Qy         1037 FPG           Qy         AAR04136           XX         XX           XX         XX           XX         XX |
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                 GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR
                                                                               QNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPL
                                                                                                     PRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLF
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994. .996
(Jabel= putative N-glycosylation site 1022. .1024
/label= putative N-glycosylation site 1045. .1047
/label= putative N-glycosylation site 1051. .1053
/label= putative N-glycosylation site 1076. .1078
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                        GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR
                                                               QNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPL
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inflammatory bowel disease; multiple sclerosis; HIV; AIDS.
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                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel isolated or recombinant modified integrin protein having extracellular domains of integrin alpha and beta subunits where one of the subunits has one or more mutations, an altered subratice feature or an amino acid substitution or internal deletion, extracellular domains of the integrin beta subunit that comprise a mutation that alters a non-cystain residue to cysteine or extracellular domains of integrin alpha and beta subunits. The polypeptide of the invention demonstrates antipsoriatic, thrombolytic, anticoagulant, osteopathic, cytostatatic, immunosuppressive, antiinflammatory, neuroprotective and antisickling activities and may be useful for immunotherapy in order to prevent or treat an integrin-mediated disorder such as an inflammatory disorder, an autoimmune disorder, thrombosis, cancer, osteoporosis, sickle cell anaemia, psoriasis and multiple subunit precursor protein of the invention.
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                                                                                                                                                                                                                                                                                                                              Novel modified integrin protein having extracellular domains of integrin alpha and beta subunits or integrin alphaII and beta3 subunit, useful for treating integrin mediated disorders.
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Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 4; 232pp; English.
                               /note= "Encoded by CCC"
   Location/Qualifiers
                                                                                                                                                      2002US-0396783P.
2002US-0396790P.
2002US-0410135P.
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98.8%;
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 Key
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17-JUL-2002; 2
11-SEP-2002; 3
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(EXPR-) EXPRESSION DIAGNOSTICS
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                                WPI; 2004-400724/37
                      Fry
                                                                                                                   Sequence 1152 AA;
                     Wohlgemuth J,
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Identifying an inhibitor of human immunodeficiency virus (HIV) entry into
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                                                                                                                                                                                                                                                                             The present invention relates to diagnosing or monitoring transplant rejection, e.g. cardiac or kidney transplant rejection, in an individual comprises detecting the expression level of one or more genes. The methods, system and kits are useful in diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, renotranical organ replacement rejection, in an individual. The method is also useful in assessing the immune status of an individual. The methods are also useful in diagnosing and monitoring diseases that involve the immune system, e.g. rheumatoid arthritis, lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or viral, bacterial or fungal infection. The present sequence represents a protein that is encoded by the mRNA of the invention.
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Pred. No. 0;
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8; Mismatches
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                                                                                   Woodward R,
2002US-00131831.
2002US-00325899.
 24-APR-2002;
20-DEC-2002;
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                                 YDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNF
                                                                                                                                                                                                                                                                                                                                                                        SLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVG
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HGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTVGAQGHVLLLRSQ
                                                                                                          PVLRVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVT
                                                                                                                                                 YDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNF
                                                                                                                                                                                                                                                                                                                        SLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEV
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The present invention describes a method (MI) for identifying an inhibitor of HIV entry into a human host cell. (MI) comprises identifying an inhibitor of a cell surface polypeptide selected from CXRR-4 (352 amino acids, SEQ ID NO:8, ADP44055), CCR7 (378 amino acids, SEQ ID NO:12, ADP44065), CDIC (1163 amino acids, SEQ ID NO:12, ADP44065), CDIC (1163 amino acids, SEQ ID NO:14, ADP44061), CDJ7 (323 amino acids, SEQ ID NO:20, ADP44067), CDJ7 (522 amino acids, SEQ ID NO:20, ADP44067), CDJ7 (566 amino acids, SEQ ID NO:22, ADP44067), CDJ7 (566 amino acids, SEQ ID NO:22, ADP44065), CSP3R (836 amino acids, SEQ ID NO:24, ADP44071), RARA (462 amino acids, SEQ ID NO:26, ADP44073), GABRIA (576 amino acids, SEQ ID NO:22, ADP44077), GABRIA (576 amino acids, SEQ ID NO:32, ADP44077), GABRIA (576 amino acids, SEQ ID NO:30, ADP44077), GABRIA (570 amino acids, SEQ ID NO:30, ADP440079), GABRI β a human host cell useful for preventing and/or treating HIV infection, identifying an inhibitor of a cell surface polypeptide such as CXCR-4. exemplification of the present invention Claim 1; SEQ ID NO 14; 133pp; English 

Sequence 1163 AA;

120 360 480 540 197 RIHFTFKEFONNPNPRSLIKPITQLLGRIHTATGLRKVVRELFNITNGARKNAFKILFLL 240 TDGEKFGDPLGYEDVIPELDREGVIRYVLGFGDAFRSEKSRQELNTVASKPPRDHVFQAN 300 GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR 420 79 FNLDTEELTAFRVDSAGFGDSVVQYANSWVVVGAPQKITAANQTGGLYQCGYSTGACEPI 61 RLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLRQQPQK FPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKELVSTIMEQLKKSKTLFSLMQYSEEF NFEALKTVQNQLREKI FAIEGTQTGSSSSFEHEMSQEGFSAAITSNGPLLSTVGSYDWAG QNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPL PRGWR-RWWCDAVLYGEQGHPWGRFGAALTVLGDVNGDKLTDVVIGAFGEEENRGAVYLF FNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSTGSCEPI 9 Indels Length 143; Mismatches 295; 58.9%; Score 3460; DB 8; 60.7%; Pred. No. 3.7e-277; Conservative Local Similarity 685; 318 80 121 378 Query Match 20 138 181 198 241 258 301 361 421 438 481 498 Best Loca Matches g рр g δ 셤  $\delta$ Db g g ð à à g  $\delta$ ò ð

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541 HGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTVGAQGHVLLLRSQ

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1019 1079 919 720 736 780 840 900 854 959 974 Mip-1(beta); Novel marker gene of inflammatory bowel disease (IBD) comprising base sequence of e.g., Fc gamma R IIIa, Fc gamma R IIIb, Mig, NRG-2, hexokinase 3, HM74, CD11c, TLR2 gene, useful for screening therapeutic SLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVG GPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEV SQGTWSTSCRINHLIFRGGAQITFLATFDVSPKAVLGDRLLLTANVSSENNTPRTSKTTF PVLRVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRDRLREGQ1QSVVT PVLWVGVSMQFIPAEIPRSAFECREQVVSEQTLVQSNICLYIDKRSKNLLGSRDLQSSVT YDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNF SGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRTNKTEF QLELPVKYAVYMVVTSHGVSTKYLNFTAS-ENTSRVMQHQYQVSNLGQRSLPISLVFLVP QLELPVKYAVYTVVSSHEQFTKYLNFSESEEKESHVAMHRYQVNNLGQRDLPVSINFWVP VRLNQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDI PFFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLPGQGAFVRSQTE TKVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMMSE 1128 marker gene; inflammatory bowel disease; IBD; FcgammaR IIIa; FcgammaR IIIb; Mig; NRG-2; hexokinase; HM74; REG III; LPAP; Mi L-selectin; EGFL6; IDO; IL-8; CD11c; TLR2; ulcerative colitis; Human inflammatory bowel disease marker - CD11c protein. Ą ADN02004 standard; protein; 1163 07-AUG-2002; 2002JP-00229705 Ä. (first entry) (SUMU ) SUMITOMO SEIYAKU WPI; 2004-209124/20. N-PSDB; ADN01990. Crohn's disease JP2004065120-A. 07-AUG-2002; sapiens 17-JUN-2004 04-MAR-2004 617 677 737 797 855 915 096 1020 1080 557 601 661 721 781 841 901 975 à qq ð g à Db à q ò a à g ð 셤 à 셤 8 

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SGALKSTSCSINHP1FPENSEVTFN1TFDVDSKASLGNKLLLKANVTSENNMFRTNKTEF
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                                    The invention comprises marker genes for inflammatory bowel disease (IBD) - FcgammaR IIIa, FcgammaR IIIb, Mig, NRG-2, hexokinase, HM74, RBG III, LDAP, Mip-1(beta), L-selectin, EGFL6, IDO, IL-8, CD1C, and TLR2 genes. The DNA and protein sequences of the invention are useful in the detection and treatment of IBD (e.g. ulcerative colitis and Crohn's disease). The present amino acid sequence represents an IBD marker
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                                                                                                                                         tch 58.6%; Score 3446; DB 8; al Similarity 60.5%; Pred. No. 5.4e-276; 683; Conservative 143; Mismatches 297;
                  Example; SEQ ID NO 27; 151pp; Japanese.
                                                                                                 protein of the invention.
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                                                                                                                                                                                                                                                                                 VRLNQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SQGTWSTSCRINHLIPRGGAQITPLATFDVSPKAVLGDRLLLTANVSSENNTPRTSKTTF
                                                                                                                                      QLELPVKYAVYMVTSHGVSTKYLNFTAS-ENTSRVMQHQYQVSNLGQRSLPISLVFLVP
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Treatment of viral esp. rhino-viral infection - by admin. of alpha subunit of p150.95 cell surface adhesion receptor, opt. together with a beta
                                                                                                                                                                                     p150,95 leucocyte adhesion receptor alpha-subunit; hairy cell leukaemia; rhinovirus.
                                 TKVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMMSE 1128
                                            p150.95 alpha subunit encoded by clone lambdaX47.
                                                                                                                                                                                                                                                                                                                /label= glycosylation site 385..387 / Jabel= glycosylation site 392..394 / Jabel= glycosylation site 697..699 / Jabel= glycosylation site 735..737 / Jabel= glycosylation site 899..901
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61. .63
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                                     FNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSTGSCEPI
                                                  FPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKELVSTIMEQLKKSKTLFSLMQYSEEF
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tch 58.6%; Score 3446; DB 8; Length 1 al Similarity 60.5%; Pred. No. 5.4e-276; 683; Conservative 143; Mismatches 297; Indels
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Clone lambda X47 was isolated from a cDNA library constructed from total NMA extracted from photobol myristate acetate stimulated HL-60 myelomonocytic cells. The library was screened with oligomucleotide probes based on tryptic peptide fragments of p150.95. The sequence can be attached to appropriate control elements and expressed in prokaryotic and expressed in prokaryotic and expressed in prokaryotic and expressed in prokaryotic and infection because it interacts with ICAM-1 and inhibits cell-virus attachment. It can also be used as an anti-inflammatory agent. See also AAQ06063.4, AAR07121.8 and AAR07122-6. (Updated on 25-WAR-2003 to correct PR field.)
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This sequence represents a human beta-integrin CDIIc subunit which is used to describe a method for identifying compounds that modulate the interaction of the beta-integrin alpha-d subunit with a binding partner of alpha-d which involves contecting an alpha-d polypeptide with an alpha d binding partner, one of which is immobilised and the other of which labelled, in the presence of a test compound, and determining if the compound affects binding between the alpha-d polypeptide is alpha-d binding partner, where the alpha-d polypeptide is alpha-d or its fragment comprising the cytoplasmic, transmembrane or extracellular domain of alpha-d. Compounds that modulate alpha-d binding could be used to treat diseases such as type-I diabetes, atherosclerosis, multiple sclerosis, asthma, psoriamis, lung inflammation, acute respiratory distress syndrome and rheumatoid arthritis
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labelled alpha-d polypeptide, useful for, e.g. treating type-I diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beta-integrin alpha-d subunit; human; modulator; treatment; psoriasis; type-I diabetes; atherosclerosis; multiple sclerosis; asthma; lung inflammation; acute respiratory distress syndrome; CD11c subunit;
                                                                                                                                                                                                                 PSFSVQBELDFTLKGNLSFGWVRQILQKKVSVVSVABITFDTSVYSQLFGQERFMRAQTT
SGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRTNKTEF
                                                            QLELPVKYAVYMVVTSHGVSTKYLNFTAS-ENTSRVMQHQYQVSNLGQRSLPISLVFLVP
                                                                               PFFGIQEEFNATIKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLPGQGAFVRSQTE
                       SOGTWSTSCRINHLIFRGGAQITFLATFDVSPKAVLGDRLLLTANVSSENNTPRTSKTTF
                                                                                                                           VRINQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDI
                                                                                                                                                                                                                                                                       TKVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMMSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human Beta-integrin CD11c subunit protein.
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94US-00362652.
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                                                                                                                     80 GLOVPPEAVNMSLGLSLASTISPSQLLACGPTVHHECGRNMYLTGLCFLLGPT--QLTQR
                                                                                                                                         FPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKELVSTIMEQLKKSKTLFSLMQYSEEF
                                                                                                                                                             LPVSRQECPRQEQDIVFLIDGSGSISSRNFATMMNFVRAVISQFQRPSTQFSLMQFSNKF
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                                                                      TDGEKFGDPLGYEDVIPELDREGVIRYVLGFGDAFRSEKSRQELNTVASKPPRDHVFQAN
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                                           Gaps
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                     Length 1163;
                                         Indels
                     3; DB 2;
4.4e-274;
                                         294:
                  58.2%; Score 3423; DE 60.2%; Pred. No. 4.4e-ive 149; Mismatches
                                        Conservative 149;
                            Similarity
Sequence 1163 AA;
                                       680;
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                   Query Match
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Integrins are a class of membrane-associated molecules that participate in cellular adhesion. Integrins are made up of an alpha subunit and a cet as subunit. One class of human integrins are restricted to expression in white blood cells and have a common beta2 subunit: the leukocyte integrins, Leu-CAMS, leukointegrins or beta2 integrins. Beta2 integrins have an important role in immune and inflammatory responses. The present protein sequence is the human integrin alpha subunit CDIC. This sequence was used in an alignment to identify a novel beta2 integrin alpha subunit: alpha d (AAA60014 and AAB07359). The present sequence has subunit: alpha d (AAA60014 and AAB07359). The present sequence has comproximately 68 identity to the protein sequence of alpha d. The CAlpha d gene and protein may be useful in therapy for diseases linked to aberrant alpha d function e.g. Type I diabetes, atherosclerosis, multiple consistness syndrome, rheumatoid arthritis and leukocyte adhesion deficiency clastress syndrome, rheumatoid arthritis and leukocyte adhesion deficiency clastress injury. The monoclonal antibodies may be used in the integrin injury. The monoclonal antibodies can also be used to detect and
PFFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLPGQGAFVRSQTE 1079
                                        system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; macrophage infiltration inhibition; alpha d integrin; leukccyte integrin; Leu-AM; leukcintegrin; immune response; inflammation; leukcoyte adhesion deficiency; LAD; Type I diabetes; atherosclerosis; multiple sclerosis; asthma; psoriasis; beta2 integrin; lung inflammation; acute respiratory distress syndrome; Crohn's disease rheumatoid arthritis; central nervous system injury; CD11c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          monoclonal antibodies to inhibit inflammation at central nervous
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and reduce
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99US-00350259.
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Score 3423; DB 3; Length 1163; Pred. No. 4.4e-274;

58.2**%**; 60.2**%**;

Search completed: November 9, 2004, 12:08:14 Job time: 109.25 secs

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9, 2004, 12:17:49; Search time 97.5 Seconds (without alignments) 4119.157 Million cell updates/sec
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(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
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                                      OM protein - protein search, using sw model
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Maximum Match 100%
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| Sequence 2, Appli                       | ٥              | 0             | 2                  | ď                   | 23           | 0         | 7                  | ۰<br>۱ | δ.   | 4                   | -     | 2. Ann | ` c         | ic      | ) C    |        | Segmenter 103 App    | 25   | , C        | ,              |           | 810                  | 10             | 10          | 25             | 25        | 33     | , (c            | 1 (0)                | 4           |
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| 9 US-09-350-259-2<br>10 US-09-891-943-2 | US-09-350-259- | 3-09-891-943- | 9 US-09-350-259-55 | 10 US-09-891-943-55 | US-09-350-25 | 0 US-09-8 | 9 US-09-350-259-37 | m      | 9    | 10 US-09-891-943-46 | 192-1 | 2      | 3-10-261-16 | 6 US-10 | US-10  | -60-SD | 10 US-09-891-943-103 | 101  | 9-891-943- | US-10-177-550- | US-10-173 | 14 US-10-291-265-810 | US-09-984-130- | -09-836-353 | US-09-918-715- | US-10-474 | 10-291 | US-09-984-130-3 | LO US-09-836-353A-35 | -10-262-839 |
| 1161                                    | 1161           | 1161          | 1161               | 1161                | 1161         | 1161      | 1151               | 1151   | 1155 | 1155                | 369   | 1170   | 1170        |         |        | -      | 494                  | 413  | 413        | 1179 1         | 1179 ]    | 1188 ]               | 1151           | 1151        | 1179 1         | 1179 1    | 1188 1 | 1189 1          | 1189 1               | 1189 1      |
| 57.6                                    | 57.4           | 57.4          | 4.                 | 54.7                | 54.4         | 4.        | 54.3               | 54.3   | 54.1 | 54.1                | 31.4  | 26.1   | 26.1        | 25.7    | 22.8   | 20.9   | 20.9                 | 19.2 | 19.2       | 19.2           | 19.2      | 18.5                 | 18.5           | 18.5        | 18.5           | 18.5      | 18.4   | 18.4            | 18.4                 | 18.4        |
| 3388<br>3388                            | 372.           | 372           |                    | 3213.5              | 3201         |           | _                  | 3192.5 | 3180 | 3180                | 1848  | 23     | 1532.5      | 1509    | 1341.5 | 1229.5 | 1229.5               | m    | 1128.5     | 1128           | 1128      |                      | 0              | 085.        | 085.           | 'n        | 1083   |                 | φ.                   | 1079.5      |
| 14<br>15                                | 16             | 17            | 18                 | 19                  | 20           | 21        | 22                 | 23     | 24   | 25                  | 26    | 27     | 28          | 29      | 30     | 31     | 32                   | 33   | 34         | 35             | 36        | 37                   | 38             | 9.0         | 40             | 41        | 42     | 43              | 44                   | 45          |

## ALIGNMENTS

61 RLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLRQQPQK 120 61 RLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCEJFGSNJRQQPQK 120 1 FNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSTGSCEPI APPLICANT: Spiringer, Timothy
APPLICANT: Spiringer, Dinachy
APPLICANT: Shimacka, Motcomu
APPLICANT: Shimacka, Julia
APPLICANT: Shimacka, Julia
APPLICANT: Mayo, Stephen
TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
FILE REFERENCE: A-70586-1/RFY/RMS/RMK
CURRENT APPLICATION NUMBER: US 60/9902,481A
CURRENT FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/216,600
PRIOR FILING DATE: 2000-07-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 3
LENGTH: 1137 DB 10; Length 1137; Indels . 0 Query Match
100.0%; Score 5879;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1137; Conservative 0; Mismatches Sequence 3, Application US/09902481A Publication No. US20030054440A1 GENERAL INFORMATION: ORGANISM: Artificial sequence FEATURE: ; OTHER INFORMATION: synthetic US-09-902-481A-3 US-09-902-481A-3 TYPE: PRT ð d à

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TDGEKFGDPLGYEDVIPELDREGVIRYVLGFGDAFRSEKSRQELNIVASKPPRDHVFQAN 300
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                    APPLICANT: Springer, Timothy
APPLICANT: Shimmaoka, Motomu
APPLICANT: Shiffman, Julia
APPLICANT: Shiffman, Stephen
TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGI
FILE REFERENCE: A-70586-1/RFT/RMS/RWK
CURRENT APPLICATION NUMBER: US/09/902,481A
CURRENT FILING DATE: 2000-07-09
PRIOR FILING DATE: 2000-07-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                        3; Mismatches
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Pred. No. 0;
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Best Local Similarity 99.5
Matches 1131; Conservative
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| Db 137 FPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRWKEFVSTVMEQLKKEKTLFSLMQYSEEF 196  Qy 181 RIHFTFKEFGNNPPRSLIKPITQLLGRTHTATGLRKVVRELFNITNGARKNAFKILFLL 240  L97 RIHFTFKEFGNNPPRSLIKPITQLLGRTHTATGLRKVVRELFNITNGARKNAFKILFLL 240  241 TDGEKFGDPLGYEDVIPELDREGVIRYUGFGDAFRSEKSRQELNTTASKPPRDHVFQNN 316  Qy 241 TDGEKFGDPLGYEDVIPELDREGVIRYUGFGDAFRSEKSRQELNTTASKPPRDHVFQNN 316  Qy 301 NFFALKTVQNQLREKIFALEGTQTGSSSSFEHEMSQEGFSAAITSNGPLLGTVGSYDWAG 376  Db 317 NFFALKTTONQLREKIFALEGTQTGSSSSFEHEMSQEGFSAAITSNGPLLGTVGSYDWAG 376  Qy 361 GVFLYTSKEKSTFINMTRYDSDWNDAYLGYAAAIILRRNVQSLVLGAPRYQHIGLVAMFR 420  Qy 421 QNTGWMESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYEQTRGGQVSVCPL 496  Qy 421 QNTGWMESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYEQTRGGQVSVCPL 496  Qy 481 PRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPHYEQTRGGQVSVCPL 496  Qy 481 PRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPHYEQTRGGQVSVCPL 496  Qy 7 PRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPHYEQTRGGQVSVCPL 556  Qy 691 HGTGSSGISPSHSORIAGSKLSPRLQYFGGSLSGGODLTMDGLVDLTVGAQGHVLLLRSQ 616  DD 557 HGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGODLTMDGLVDLTVGAQGHVLLLRSQ 616   | 66<br>77<br>73<br>77<br>88<br>77<br>10<br>10<br>10<br>10<br>10<br>10<br>10 | RESULT 4 US-09-902-481A-1 ; Sequence 1, Application US/09902481A ; Publication No. US20030054440A1 ; GENERAL INFORMATION: ; APPLICANT: Springer, Timothy   |
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| Qy         721 SINGTPLSAFGNIRPULAEDAQRIETALFPERNCCANDNICQDDLSITFSFMSLDCLVVG 780           Db         721 SINGTPLSAFGNIRPULAEDAQRIETALFPERNCCANDNICQDDLSITFSFMSLDCLVVG 780           Qy         781 GPREFNVTYTVRNDGEDSYRTQVTFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEV 840           Db         781 GPREFNVTYTVRNDGEDSYRTQVTFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEV 840           QY         841 SGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMFRTNKTFF 900           Db         841 SGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMFRTNKTFF 900           QY         901 QLELPVKYAVYWVTSHGVSTKYLNFTASENTSRVMQHQYQVSNLGQRSLPISLVFLVPV 960           Db         901 QLELPVKYAVYWVTSHGVSTKYLNFTASENTSRVMQHQYQVSNLGQRSLPISLVFLVPV 960           QY         901 QLELPVKYAVYWVTSHGVSTKYLNFTASENTSRVMQHQYQVSNLGQRSLPISLLVFLVPV 960           QY         901 QLELPVKYAVYWVTSHGVSTKYLNFTASENTSRVMQHQYQVSNLGQRSLPISLLVFLVPV           Db         901 QLELPVKYAVYWVTSHAVSTKZLPHABLERRAPVYNCSIAVCRIQCDIP 1020           QY         961 RLNQTVIWDRPQVTFSBNLSSTCHTKERLPSHSPELAELRRAPVYNCSIAVCRIQCDIP 1020           QY         1021 FFGIQEBFNATLKGNLSFDWYIKTSHNHLLIVSTABILLENDSVFTLLPGQGAFVRSQTET 1080           Db         1021 FFGIQEBFNATLKGNLSFDWYIKTSHNHLLIVSTABILENDSVFTLLPGQGAFVRSQTET 1080           QY         1021 FFGIQEBFNATLKGNLSFDWYIKTSHNHLLIVSTABILENDSVFTLLPGQGAFVRSQTET 1080           QY         1021 FFGIQEBFNATLKGNLSFDWYIKTSHNHLLIVASTABILENDSVFTLLPGQGAFVRSQTET 1080           DD         1021 FFGIQE | RESULT 3   Sequence 3, Application US/09350259                             | Qy         61 RLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLRQQPQK 120           Db         77 RLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLRQQPQK 136           Qy         121 FPEALRGCPQEDSDIAFLIDGSGS11PHDFRRWKELVSTIMEQLKKGKTLFSLMQYSEEF 180           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII |

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Publication No. US20030077278A1

GERERAL INFORMATION:

APPLICANT: Gallatin, Michael W.

APPLICANT: Van der Vieren, Monica

TITLE OF INVENTION: No. US20030077278A1el Hum

TITLE OF INVENTION: No. US20030077278A1el Hum

CURRENT APPLICATION NUMBER: US/09/891,943

CURRENT FILING DATE: 1999-11-16

PRIOR APPLICATION NUMBER: 09/193,043

PRIOR PILING DATE: 1994-08

PRIOR PILING DATE: 1994-12-21

PRIOR PILING DATE: 1994-12-21

PRIOR PILING DATE: 1994-12-21

PRIOR PILING DATE: 1994-12-21

PRIOR PILING DATE: 1994-10-03

NUMBER: OF SEQ ID NOS: 114

SOFTWARE: PatentIN Ver. 2.0
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  APPLICANT: Shimaoka, Motomu
APPLICANT: Shifman, Julia
APPLICANT: Shifman, Julia
APPLICANT: MAYO, STEDANE MAYO, STEDANE
TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
FILE REFERENCE: A-70586-1/RFT/RMS/RMK
CURRENT PILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/216,600
PRIOR APPLICATION NUMBER: US 60/216,600
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Version 3.1
SEQ ID NO 1
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8; Mismatches
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Pred. No. 0;
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Best Local Similarity 98.9*
Matches 1124; Conservative
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; LOCATION: (17)..()
; OTHER INFORMATION:
US-09-902-481A-1
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Pred. No. 0;
8; Mismatches
   FILE REFERENCE: 00786-548001
CURRENT APPLICATION NUMBER: US/10/144,259
CURRENT FILING DATE: 2002-09-04
FRIOR APPLICATION NUMBER: US 09/758,493
PRIOR FILING DATE: 2001-01-11
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 30
TYPE: PRI
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Best Local Similarity 98.9
Matches 1124; Conservative
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Publication No. US20030109691A1
GENERAL INFORMATION:
APPLICANT: Arnaout, M. Amin
APPLICANT: Li, Rui
APPLICANT: Li, Rui
APPLICANT: Xiong, Jian-Ping
TITLE OF INVENTION: VARIANT INTEGRIN POLYPEPTIDES AND USES THEREOF
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               QNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPL
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Publication No. US2030054440A1

Publication No. US2030054440A1

GENERAL INFORMATION:

APPLICANT: Sprimacka, Motomu

APPLICANT: Shifman, Julia

APPLICANT: Shifman, Julia

APPLICANT: Shifman, Julia

APPLICANT: MAYO. Stephen

TILLE REFERENCE: A-70586-1/RFT/RMS/RMK

CURRENT PELLING NUMBER: US/09/902,481A

CURRENT FILING DATE: 2001-07-09

PRIOR FILING DATE: 2000-07-07

NUMBER OF SEQ ID NOS: 7

SOFTWARE: Patentin version 3.1

SEQ ID NO 5.
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ORGANISM: Artificial sequence
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CURRENT APPLICATION NUMBER: US/10/207,655
NUMBER: OF SID NOS: 426
SOFTWARE: Patentin version 3.0
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Publication No. US20030118592A1
GENERAL INFORMATION:
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Best Local Similarity 98.9%;
Matches 1124; Conservative
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US-10-207-655-176
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US-10-207-655-176
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LENGTH: 1153
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                                                                       FPEALKGCPQEDSDIAFLIDGSGSIIPHDFRRMKELVSTIMBQLKKSKTLFSLMQYSEEF
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APPLICANT: Shimaoka, Motomu
APPLICANT: Shimaoka, Motomu
APPLICANT: Shiman, Julia
APPLICANT: Shiman, Julia
APPLICANT: Shiman, Julia
TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
FILE REPRENCE: A-70586-1/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/902, 481A
CURRENT FILING DATE: 2001-07-09
PRIOR PLING DATE: 2000-07-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
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                                                                                                              ; Sequence 6, Application US/09902481A; Publication No. US20030054440A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           99.2%;
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Best Local Similarity 98.7*
Matches 1122; Conservative
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; Garent No. US20020123614A1
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; Garent No. US20020123614A1
; APPLICANT: Springer, Timothy A.
; APPLICANT: Shimaoka, Motomu
; APPLICANT: Lu, Chafen
; TITLE OF INVENTION: MODIFIED POLYPEPTIDES STABILIZED IN A.
; TITLE OF INVENTION: DESTRED CONFORMATION AND METHODS FOR PRODUCING SAME
; FILE REFERENCE: CBN-002CP
; CURRENT APPLICATION NUMBER: US/09/945,265
; CURRENT APPLICATION NUMBER: US/09/945,265
; CURRENT APPLICATION NUMBER: US/09/945,265
; RIOR APPLICATION NUMBER: US/09/945,265
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
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                                                                                                                                                                         YDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNF
PRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLF
                                                                                                       PVLRVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVT
                                   HGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTVGAQGHVLLLRSQ
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Pred. No. 0;
8; Mismatches
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TYPE: PRT
ORGANISM: HOMO
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Best Local Simi
Matches 1123;
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YDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNF
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ilarity 60.2%; Pred. No. 1.1e-282;
Conservative 149; Mismatches 294;
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APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. US20020062008Alel Hum
TITLE FERENCE: 27866/3504
CURRENT APPLICATION NUMBER: US/09/350,259
CURRENT FILING DATE: 1999-07-08
EARLIER FILING DATE: 1999-11-16
EARLIER FILING DATE: 1999-11-16
EARLIER FILING DATE: 1993-12-23
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-12-21
EARLIER APPLICATION NUMBER: 08/36,652
EARLIER PILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/09350259
Patent No. US20020062008A1
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                                       Sequence 204, Application US/10116275

Publication No. US20030211476A1

GENERAL INFORMATION:

APPLICANT: Blayden, David

APPLICANT: Brayden, David

APPLICANT: Brayden, David

APPLICANT: Higgins, Lisa

TITLE OF INVENTION: Compositions Targeting Peyer's Patches and Methods and

TITLE OF INVENTION: Compositions Targeting Peyer's Patches and Methods and

TITLE OF INVENTION: Compositions Targeting Peyer's Patches and Methods and

TITLE OF INVENTION: Compositions Targeting Peyer's Patches and Methods and

TITLE OF INVENTION: Compositions Targeting Peyer's Patches and Methods and

TITLE REFERENCE: E1067/20087

CURRENT APPLICATION NUMBER: US/10/116,275

NUMBER OF SEQ ID NOS: 349

SEQ ID NOS: 349

SEQ ID NOS: 349

SEQ ID NOS: 204
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                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-275-204
        RESULT 11
US-10-116-275-204
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          PPEALRGCPOEDSDIAFLIDGSGSIIPHDFRRMKELVSTIMEQLKKSKTLFSLMQYSEEF
                                    RIHFTFKEFQNNPNPRSLIKPITQLLGRTHTATGLRKVVRELFNITNGARKNAFKILFLL
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RESULT 13 US-09-891-943-4 ; Sequence 4, Application US/09891943

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GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Michael W.
TITLE OF INVENTION: No. US20030077278A1el Human 2
FILE REFERENCE: 27866/38004
CURRENT APPLICATION NUMBER: US/09/891,943
CURRENT APPLICATION NUMBER: 09/193,043
PRIOR FILING DATE: 1998-11-16
PRIOR PILING DATE: 1998-11-16
PRIOR FILING DATE: 1994-08-05
PRIOR FILING DATE: 1994-12-21
PRIOR FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PARCHILIN Ver. 2.0 Query Match 58.2%; Score 3423; DB 10; Best Local Similarity 60.2%; Pred. No. 1.1e-282; Matches 680; Conservative 149; Mismatches 294; LENGTH: 1163 TYPE: PRT ORGANISM: Homo sapiens US-09-891-943-4 121 181 198 241 258 301 318 361 421 438 481 498 541 557 601 g g  $\delta$ 셤  $\overset{\sim}{\circ}$ D ď qq à qq ò g ò a ð g à a 셤 ð ð ò

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; ORGANISM: Homo sapiens
US-09-350-259-2
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APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: NO. US20030077278Alel Human 2
FILE RPERENCE: 27866/35004
CURRENT APPLICATION NUMBER: U$/09/891,943
CURRENT FILING DATE: 2001-06-26
PRIOR PELICATION NUMBER: 09/133,043
PRIOR FILING DATE: 1998-11-16
PRIOR FILING DATE: 1994-08-05
PRIOR PLICATION NUMBER: 08/362,652
PRIOR APPLICATION NUMBER: 08/362,652
PRIOR PLING DATE: 1994-08-05
PRIOR PLING DATE: 1994-12-21
PRIOR FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PALENTIN Ver. 2.0
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TYPE: PRT
ORGANISM: Homo sapiens
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                                                      SLVREPIPSPONIRPVLAVGSQDLFTASLPFERNCGQDGLCEGDLGVTLSFSGLQTLTVG
                                                                                                               SGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRTNKTEF
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                                                                                            GPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEV
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Search completed: November 9, 2004, 12:46:48 Job time : 102.5 secs

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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on:

November 9, 2004, 11:57:57; Search time 23 Seconds

(without alignments)

3278.416 Million cell updates/sec

Title:

US-09-902-481B-3

Perfect score: 5879
Sequence:

1 FNLDTENAMTFQENARGFGQ......FKRQYKDMMSEGGPPGAEPQ 1137

Scoring table:

BLOSUM62

Gapop 10.0, Gapext 0.5

Searched:

478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Issued patents AA:\*

| cgn2\_6/ptodata1/liaa/5A\_COMB.pep:\*
| cgn2\_6/ptodata1/liaa/6A\_COMB.pep:\*
| cgn2\_6/ptodata1/liaa/6A\_COMB.pep:\*
| cgn2\_6/ptodata1/liaa/BaCOMB.pep:\*
| cgn2\_6/ptodata1/liaa/BaCOMB.pep:\*
| cgn2\_6/ptodata1/liaa/PCTUS COMB.pep:\*
| cgn2\_6/ptodata1/liaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Appli 5424399 Sequence 44, Appl Sequence 44, Appl Sequence 43, 7 Sequence 43, 7 Patent No. 5424 Sequence 4, Sequence 4, Sequence 4, Sequence 4, Sequence 2, Sequence 2, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Description Sequence 4 Sequence 4 Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence US-08-485-618-3 US-08-60-672-3 US-08-60-672-3 US-08-943-363-3 US-09-193-043-3 US-09-193-043-3 US-09-360-255-3 US-08-476-062A-43 US-08-476-062A-43 US-08-286-889-4 US-08-485-618-4 US-08-362-652-4 US-08-605-672-4 US-08-943-333-4 5424399-2 US-08-476-062A-44 PCT-US96-01314-44 US-08-173-497-4 US-09-350-259-4 US-08-173-497-2 US-08-286-889-2 SUMMARIES Query Match Length DB 1153 11153 11153 11153 11153 11153 11163 11163 11163 11163 11163 1163 5839 5839 5839 5839 5839 5808.5 5808.5 3446 5839 5839 33 88888 3446 Result 

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99.3%; Score 5839; DI 98.9%; Pred. No. 0; tive 8; Mismatches

Best\_Local Similarity 98.9%; Matches 1124; Conservative

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Query Match

Length 1153; Indels 60

1 FNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSTGSCEPT

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|                  | aorianhac    | Seguence        | Sequence        | Seguence         | Seguence        | Sequence        | Sequence         | Seguence        | Seguence         | Seguence         | Sequence          | Seguence         | Sequence         | Sequence          | Sequence         | Sequence         | Seguence          | Sequence         |
| 710_00 40E 610 0 | 7-9-50-50-50 | US-08-362-652-2 | US-08-605-672-2 | US-08-482-293A-2 | US-08-943-363-2 | US-09-193-043-2 | US-09-688-307A-2 | US-09-350-259-2 | US-08-485-618-99 | US-08-605-672-99 | US-08-482-293A-99 | US-08-943-363-99 | US-09-193-043-99 | US-09-688-307A-99 | US-09-350-259-99 | US-09-193-043-55 | US-09-688-307A-55 | US-09-350-259-55 |
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## LIGNMENT

RESULT 1

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US-08-173-497-3

US-08-173-497-3

Sequence 3, Application US/08173497

Sequence 3, Application US/08173497

Sequence 3, Application US/08173497

Sequence 3, Application US/08173497

APPLICANT Gallatin, W. Michael

APPLICANT Gallatin, W. Michael

APPLICANT Gallatin, W. Michael

APPLICANT WORNEYLOW: No. 5437958el Human 2 Integrin Alpha

TITLE OF INVENTION: No. 5437958el Human 2 Integrin Alpha

TITLE OF INVENTION: Subunit

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ARREFT: 233 S. Wacker Drive, 6300 Sears Tower

CITY: Chicago

STREET: 111inois

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: BACENTIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/173,497

ATLING DATE: Patentin S. 35,302

ATTORNEY/AREAT INFORMATION:

REGISTRATION INFORMATION:

REGISTRATION INFORMATION:

REGISTRATION INFORMATION:

TELEFRAX: 312-474-6300

TELEFRAX: 312-474-6300

TELEFRAX: 312-474-6300

TELEFRAX: 312-474-0448

TELECOMMUTCATION INFORMATION:

TRELEMENT OR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1153 maino acids

TYPE: amino acid

STRANDENSS: single

MOLECULE TYPE: protein

US-08-173-497-3
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TOPOLOGY: lin
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TELEFAX: 3:
RESULT 2
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                                                           APPLICANT: Gallatin, W. Mich
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5470953el Human 2 Integrin
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSE: Marehall, O'Toole, Gerstein, Murray & STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,889
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Pred. No. 0;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: P38,659 REFERENCE/DOCKET NUMBER: 27866/32168 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                    CITY: Chicago STATE: Illinois COUNTRY: United States COUNTRY: United States ZIP: 60606-6402 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk CONFUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
ATTORNEY/AGENT INFORMATION:
    US/08286889
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98.9%;
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids
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Sequence 3, Application Patent No. 5470953 GENERAL INFORMATION:
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               SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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98.9%; Pred. No. 0;
ive 8; Mismatches
                                                                                                                    APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
APOLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                 27866/32797
                                                   US/08/485,618
PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                           NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 2:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1153 amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                 APPLICATION NUMBER: FILING DATE:
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                                                                                                       QNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPL
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         GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR
                                GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR
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APPLICANT: Gallatin, W. Michael
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5728533e1 )
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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; Sequence 3, Application US/08485618
; Patent No. 5728533
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GPREFNUTVIVENDGEDSXRIQVIFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEV
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Pred. No. 0;
                    27866/32391
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 2786
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEFX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids
                                                                                                                                                                                                                                                                     99.3%;
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Matches 1124; Conservative
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TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                               amino acid
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CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
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APPLICATION NUMBER: US/08/362,652
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/08362652
Patent No. 5766850
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 576685061
NUMBER OF SEQUENCES: 93
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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STATE: Illinois
COUNTRY: United States
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US-08-362-652-3
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  Length 1153;
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Score 5839; D
Pred. No. 0;
8; Mismatches
99.3%;
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257 IDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVN
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; Sequence 3, Application US/08943363
; Patent No. 5837478
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                            FFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLPGQGGAFVRSQTET 1096
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                                                                       KVEPPEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDWMSEGGPPGAEPQ 1137
                                                                                                KVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMMSEGGPPGAEPQ 1153
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e, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                             STATE: Illinois
CONNTRY: United States
ZIP: 6060-6402
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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Pred. No. 0;
8; Mismatches
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APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5831029el Human
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27866/32684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY AGENT INFORMATION:
NAME: Williams Jr., JOSEPH A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/482,293A
                                                                                                                                                                                                                                                                                                                               3: Marshall, O'Toole, Ge
233 South Wacker Drive,
                                                                                                                                                                                          Sequence 3, Application US/08482293A Patent No. 5831029
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312-474-0448
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INFORMATION FOR SEQ ID NO:
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STRANDEDNESS: sir
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CLASSIFICATION:
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STREET: 23
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Best Local Simi
Matches 1124;
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US-08-482-293A-3
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APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Voeren, Monica
TILE APPLICANT: Van der Voeren, Monica
FILE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/193,043
CURRENT FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: 08/173,497
EARLIER FILING DATE: 1993-12-23
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1994-10-03
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US-09-193-043-3
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              APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 114
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233 South Wacker Drive, 6300 Sear Tower
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,363
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8; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UNDRER: US 08/173,497
FILING DATE: 23-DBC-1993
FILING DATE: 5-AUG-1994
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DBC-1994
ATTOCNEY/AGENT INFORMATION:
NAME: Williams JT., JOSEPH A.
                                                                                                           CITY: Chicago
STATE: 111inois
CUVIRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                     US/08/943,363
Gallatin, W. Michael
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TELECOMMUNICATION:
TELEPHONE: 312-474-6300
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INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids
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312-474-0448
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Best Local Similarity 98.9
Matches 1124; Conservative
                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall,
STREET: 233 South Wac
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Patent No. 6432404
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APPLICANT: Gallatin, Michael W.
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Best Local Similarity 98.9%;
Matches 1124; Conservative
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US-09-688-307A-3
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8; Mismatches
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Best Local Similarity 98.9%;
Matches 1124; Conservative
            NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patentin Ver. 2.0
                                                                ; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-193-043-3
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       EARLIER FILING DATE: 1994-12-21
EARLIER APPLICATION WUMBER: 08/943,363
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SEQ ID NO 33 LENGTH: 153
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Patent No. 6620915
GENERAL INFORMATION:
PAPPLICANT: Gallatin, Michael W.
TITLE OF INVENTION: No. 6620915el Human 2
FILE REFRENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/350,259
CURRENT FILING DATE: 1999-07-08
EARLIER APPLICATION NUMBER: 09/193,043
EARLIER APPLICATION NUMBER: 09/173,497
EARLIER FILING DATE: 1998-11-16
EARLIER FILING DATE: 1998-12-3
EARLIER FILING DATE: 1998-12-3
EARLIER FILING DATE: 1998-16-6
EARLIER FILING DATE: 1998-16-6
EARLIER FILING DATE: 1998-16-6
EARLIER FILING DATE: 1993-12-3
EARLIER FILING DATE: 1993-12-3
EARLIER APPLICATION NUMBER: 08/266,889
EARLIER FILING DATE: 1994-08-05
EARLIER APPLICATION NUMBER: 08/362,652
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| Qy   IFILDTENAMTFOENARGFGOSYVOLOGSRVVVGAPQELVAANORGSLYQCDYSTGSCEPI 60   IFILDTENAMTFOENARGFGOSYVOLOGSRVVVGAPQELVAANORGSLYQCDYSTGSCEPI 76   IFILDTENAMTFOENARGFGOSVVOLOGSRVVVGAPQELVAANORGSLYQCDYSTGSCEPI 76   IFILOVPVEANNMELGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLRQQPQK 120   IFILOVPVEANNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLRQQPQK 136   IFILOVPVEANNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLRQQPQK 136   IFILIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIH | 301 NPEA<br>317 NFEA<br>361 GVFI<br>377 GVFI<br>421 ONTC   | SNANN KGIQLGATEGASLCS VIVES KASILISATII GARII ILGANIA GARGEDNEGAVXLE WQCDAVLYGEQQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVXLE WQCDAVLYGEQQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVXLE WGCDAVLYGEQQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEDNRGAVXLE WISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTWDGLVDLTVGAQGHVLLRSQ ILSPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTWDGLVDLTVGAQGHVLLLRSQ ILSPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTWDGLVDLTVGAQGHVLLLRSQ ILSPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTWDGLVDLTVGAQGHVLLLRSQ ILSPSHSQRIAGSKLSPRLQYFGGSLSGGQDLTWDGLVDLTVGAQGHVLLLRSQ ILSPSHSQRIAGSKLSPRLQYFGGSLSGGQDLTWDGLVDLTVGAQGHVLLLRSQ ILSPSHSQRIAGSKLSGGGDVVKGKEAGEVRVCLHVQKSTRDRLKEGQIQSVYT | 616 PULRUKALIMEFNPREVARNVFECNDQVVKGREAGEVRVCLHVQKSTRDRLREGQIQSVVT 67 661 YDLALDSGRPHSRAVFNETRNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNF 72 676 YDLALDSGRPHSRAVFNETRNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNF 73 721 SLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVG 78 736 SLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVG 79 736 SLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVG 79 | OY 781 GPREPNUTVIVANDGEDSYRIQUIFFPLDLSYRKUSTLONGRSORSWRLACESASSTEV 840  DE 796 GPRESNUTVIVANDGEDSYRIQUIFFPLDLSYRKUSTLONGRSORSWRLACESASSTEV 845  OY 841 SGALKSTSCSINHPIFPRNSEVTFNITFDVDSKASLGNKILLKANVTSENNMPRTNKIEF 910  DD 856 SGALKSTSCSINHPIFPRNSEVTFNITFDVDSKASLGNKILLKANVTSENNMFRTNKIEF 915  OY 901 QLELPVKYAVVWVTSHGVSTYRNITFDVDSKASLGNKILLKANVTSENNMFRTNKIEF 915  OY 901 QLELPVKYAVVWVTSHGVSTKYLNFTASENTSRVMQHQYQVSNLGQRSLPISLVPLVPV 960 | SLV<br>ORJ<br>ORJ<br>FVF   |
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| Db 857 SGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRTNKTEF 916  Qy 901 QLELPVKYAVYMVVTSHGVSTKYLNFTASENTSRVMQHQYQVSNLGQRSLPISLVFLVPV 960  | RESULT 11  US-08-476-062A-43  j Sequence 43, Application US/08476062A  j Sequence 43, Application US/08476062A  j GENERAL INFORMATION: | STREET: 225 Franklin Street CITY: Boscon STATE: MA COUNTRY: US ZIP: 02110-2804 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM Compatible OPERATING SYSTEM: Windows 95 SOFTWARE: FastSEQ for Windows Version 2.0   | ## APPLICATION NUMBER: US/08/476,062A ### APPLICATION NUMBER: US/08/476,062A ### FILING DATE: 07-JUN-1995 ### APPLICATION NUMBER: 08/216,081 ### APPLICATION NUMBER: 07/637,830 ### APPLICATION NUMBER: 07/637,830 ### APPLICATION NUMBER: 07/639,842 ### APPLICATION NUMBER: 07/539,842 ### APPLICATION NUMBER: 07/539,842 ### APPLICATION NUMBER: 07/539,842 #### APPLICATION NUMBER: 07/539,842                       | FILING DATE: 28-UN-1988  ATTORNEY/AGENT INFORMATION: NAME: Freeman, John W. REGISTRATION NUMBER: 29,066 REFERENCE/DOCKET NUMBER: 00786/068003 TELECOMMUNICATION INFORMATION: TELEFAX: 20154 TELEFAX: 20154 TELEFAX: 20154 TELEX: 20154 TELEX: 20154   | SEQUENCE CHARACTERISTICS:  LENGTH: 1152 amino acids  TYPE: amino acid  TYPE: amino acid  TOPOLOGY: linear  MOLECULE TYPE: protein  FRACMENT TYPE: internal  Guery Match  Query Match  Best Local Similarity 98.6%; Pred. No. 0;  Matches 1121; Conservative 8; Mismatches 7; Indels 1; Gaps 1; |

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961 RLNQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLABLRKAPVVNCSIAVCQRIQCDIP 1020
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                                                                                                                                              PRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLF
                                                                                    QNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYBQTRGGQVSVCPL
                                                                                                                                                                                                                          GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR
                                                                                                                                                                            PRG-RARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLF
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TITLE OF INVENTION: HUMAN CR3a/b HETERODIMERS
NUMBER OF SEQUENCES: 12
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/78,871
FILING DATE: 16-JUN-1993
PRIOR APPLICATION NATA:
APPLICATION NUMBER: 539,842
FILING DATE: 18-JUN-1990
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FILING DATE: 28-JUN-1988
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;Patent No. 5424399
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Length 1152;
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                                                                                                                    APPLICANT: M. Amin Arnaout
TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN
TITLE OF INVENTION: ANTAGONISTS
TITLE OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 5;
                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 5808.5;
Pred. No. 0;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                PCT/US96/01314
                                                                                         Sequence 43, Application PC/TUS9601314 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US96/0:
FILING DATE: 30-JAN-96
PRIOR APPLICATION DATE:
APPLICATION NUMBER: 08/380,167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: John W. Freeman
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43:
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ATTORNEY/AGENT INFORMATION:
NAME: John W. Freeman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (617) 542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity 98.6
Matches 1121; Conservative
                                                                                                                                                                                                                           CITY: Boston
STATE: Massachusetts
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                                                           RESULT 12
PCT-US96-01314-43
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PCT-US96-01314-43
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Best Local (
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                            1081 KVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMMSEGGPPGAEPQ 1137
                                                 121 FPBALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKELVSTIMEQLKKSKTLFSLMQYSEBF
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CONTROLLING CELLULAR IMMUNE/INFLAMMATORY
RESPONSES WITH BETA2 INTEGRINS
53
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                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: 15M COMPUTED: COMPUTER: OPERATING SYSTEM: Windows 95 GOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: 08/216,081 APPLICATION NUMBER: 08/216,081 APPLICATION NUMBER: 07/637,830 FILING DATE: 04-JAN-1991 APPLICATION NUMBER: 07/539,842 FILING DATE: 18-JUN-1990 APPLICATION NUMBER: 07/212,573 FILING DATE: 28-JUN-1980 APPLICATION NUMBER: 07/212,573 FILING DATE: 28-JUN-1980 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEFHONE: 617/542-5070
TELEFHONE: 617/542-8906
TELEFHONE: 617/542-8906
                                                                                                                                                                                                                                                                 P.C.
                                                                                                                                                                                         TITLE OF INVENTION: CONTROLLING C
TITLE OF INVENTION: RESPONSES WII
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                         Sequence 44, Application US/08476062A Patent No. 5877275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29,066
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                        ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Freeman, John W REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: protein US-08-476-062A-44
                                                                                                                                                         Patent No. 5877275
GENERAL INFORMATION:
APPLICANT: Arnaout,
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                                                                                                                RESULT 14
US-08-476-062A-44
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                                                                 1096
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                                                      FNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSTGSCEPI
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                         7;
           Pred. No. 0;
3; Mismatches
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                              Conservative
            Best Local Similarity
                              Matches 1121;
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Fish & Richardson 5 Franklin Street

225 Franklin Massachusetts

Boston

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COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/01314
FILING DATE: 30-JAN-96
FRICH APPLICATION DATA:
APPLICATION NUMBER: 08/380,167
FILING DATE: 30-JAN-95
ATTORNEY/AGENT INPORMATION:
NAME: John W. Freeman
                                                                                                                                                                                                                   REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                      TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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        ADDRESSEE:
STREET: 22
CITY: Bost
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PCT-US96-01314-44
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                                                                                         GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR 420
                                                                                                                                  VRLNOTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDI 1019
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                                                                           20 FNLDTEELTAFRUDSAGFGDSVVQYANSWVVGAPQKITAANQTGGLXQCGYSTGACEPI
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                                    9
      Length 1163;
                                  Indels
                               Conservative 143; Mismatches 297;
    58.6%; Score 3446; DB 5; 60.5%; Pred. No. 5.1e-278;
             Similarity
Query Match
Best Local Simil
Matches 683; (
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IDENTIFYING INTEGRIN

RESULT 15
PCT-US96-01314-44
; Sequence 44, Application PC/TUS9601314
; GENERAL INFORMATION:
; APPLICANT: M. Amin Arnaout
; TITLE OF INVENTION: METHODS FOR IDENT;
; TITLE OF INVENTION: ANTAGONISTS
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:

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960 VRINGTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDI 1019
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                                                                  781 GPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEV 840
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         SGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRTNKTEF
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                                            797 SNLELNAEVMVWNDGEDSYGTTITFSHPAGLSYRYVAEGQKQGQLRSLHLTCDSAPVG--
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- protein search, using sw model OM protein

9, 2004, 11:57:37; Search time 27.25 Seconds (without alignments) 4014.622 Million cell updates/sec November Run on:

US-09-902-481B-4

5884 1 FNLDTENAMTFQENARGFGQ.....FKRQYKDNMSEGGPPGAEPQ 1137 score: Sequence: Title: Perfect

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

283416

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pirl:\*
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4: pir4:\* PIR 79:\* Database

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| SUMMARIES | ΙD             | RWHULB             | 800551        | RWHU1C      |         | 156126    | A53213 | A45226 | 145914   | S44142    | A35854 | A33998  | A41131    | S06046 | I58409  | T31437         | JC7294  | A35761 | 155534  | 844250 | A36108  | T10050  | A38457  | A27079    | B36429 | 002     | A27421   | 154      | 651  | 031    |
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| integrin alpha-2h | nosition-andries | integrin alpha-7 c | alpha-7 integrin - | alvoorotein IIb - | Jenkocyte adhesion | integrin almba cha | F54F2 1 protein = | integrin alpha # A | hymothetical prote | integrin alpha cha | integrin alpha cha | altroprotein TTh | jarcopiocem in in integrin almba cha | almonmotoin TTh | integrin alpha-1 |
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| A34269            | A29637           | JC5950             | 161186             | A60163            | B30892             | S38783             | S44824            | 860571             | 528277             | T09403             | T09433             | 136916           | T18523                               | T36917          | A55348           |
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| 1039              | 1394             | 1137               | 1135               | 1037              | 126                | 1106               | 1226              | 1045               | 1139               | 1115               | 1115               | 764              | 1086                                 | 604             | 272              |
| 8.4               | 8.4              | 8.3                | 8.3                | 8.3               | 8.3                | 8.0                | 7.9               | 7.7                | 7.6                | 7.2                | 7.2                | 9.9              | 5.3                                  | 5.1             | 6.4              |
| 495.5             | 494              | 489                | 488                | 486.5             | 486                | 470                | 462               | 453                | 444.5              | 426                | 421.5              | 391              | 309.5                                | 299             | 286.5            |
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Wilternate names: complement receptor type 3 alpha chain; leukocyte adhesion protein M. WiAlternate names: complement receptor type 3 alpha chain; leukocyte adhesion protein M. eukocyte integrin alpha chain; neutrophil adherence receptor alphaM chain C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence revision 31-Dec-1992 #text\_change 09-Jul-2004
C;Accession: A31108; A28915; A41600; A30892; A32218; A46526; A26091; I52567
R;Corbi, A.L.; Kishimoto, T.K.; Miller, L.J.; Springer, T.A.
J. Biol. Chem. 263, 12403-12411, 1988
A;Title: The human leukocyte adhesion glycoprotein Mac-1 (complement receptor type 3, C.

A; Reference number: A31108; MUID:88315033; PMID:2457584

A; Accession: A31108

A.Molecule type: mRNA
A.Residues: 1-1153 <COR>
A.Residues: 1-1153 <COR>
A.Residues: 1-1153 <COR>
A.Cross-references: UNIPROT:P11215; GB:J03925; NID:g187284; PIDN:AAA59544.1; PID:g307148
A.Note: part of this sequence was confirmed by protein sequencing
B.Arnaout, M.A.; Gupta, S.K.; Pierce, M.W.; Tenen, D.G.
J. Cell Biol. 106, 2153-2158, 1988
A.Title: Amino acid sequence of the alpha subunit of human leukocyte adhesion receptor hareference number: A28915; MUID:88257215; PMID:2454931

A; Accession: A28915

A, Cossereferences: 13. Sohro.

A, Cross-references: GB: M76724; NID:g180018; PIDN:AAAB8410.1; PID:g553215

B. Arnaout, M.A.; Remold-O'Donnell, E.; Pierce, M.W.; Harris, P.; Tenen, D.G.

Proc. Natl. Acad. Sci. Us.A. 85, 2776-2780, 1988

A, Title: Molecular cloning of the alpha-subunit of human and guinea pig leukocyte adhes; A, Reference number: A94193; MUID:88190151; PMID:2833753

A, Accession: A30892

A, Residues: 917-1042 - AR2.

A, Residues: Soi. U.S.A. 86, 257-261, 1989

A, Title: DAM sequence for the alphaM subunit of the human neutrophil adherence recepton A, Reference number: A32218; MUID:89098893; PMID:2563162

A;Molecule type: mRNA A;Residues: 9-1153 <HIC> A;Cross-references: GB:J04145; NID:g189068; PIDN:AAA59903.1; PID:g386975

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A, Molecule type: DNA
A, Residues: 1-1153 <PYT>
A; Cross-references: UNIPPOT: P05555; EMBL: X07640; NID: 952982; PIDN: CAA30479.1; PID: 9529
A; Note: the authors translated the codon CAC for residue 569 as Gln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVG
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                                       117 NFBALKTIQNQLREKIFAIEGTQTGSSSSFEHEMSQEGFSAAITSNGPLLSTVGSYDWAG
                                                                                                       GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR
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PMID:3044779
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A.Fitle: Amino acid sequence of the murine A.Reference number: S00551; MUID:88312584; A.Accession: S00551
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A; Residues: 1-499,501-1153 <FIE>
A; Residues: 1-499,501-1153 <FIE>
A; Ross-references: GB:S52227; NID:g263047; PIDN:AAB24821.1; PID:g263049
A; Note: the last three bases of intron 13, CaG, are included in some but not all mature A; Note: the last three bases of intron 13, CaG, are included in some but not all mature A; Note: the last thread from NCBI backbone (NCBIP:121963)
A; Note: the last three as 874, 368-371, 1986
A; Tereira Biophys. Acts 874, 368-371, 1986
A; Tereira Nacesion: A26031
A; Molecule type: protein
A; Residues: 17-31 <PIE>
A; Rosmarin, A.G.; Tenen, D.G.
B; PiPhi, H.L.; Rosmarin, A.G.; Tenen, D.G.
B; A; Recence number: 152567
A; Recence number: 152567
A; Recence of the myeloid-specific CD11b promoter.
A; Rocession: 152567
A; Residues: 1-9 <RES>
A; Residues: 1-9 <RES>
A; Residues: 1-9 <RES>
A; Cross-references: GB:M84477; NID:g180184; PIDN:AAAS1960.1; PID:g553219
C; Comment: A common beta chain (CD18) forms a heterodimer with this chain to form Mac-1
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A,Map position: 16p11.2-16p11.2
A,Map position: 16p11.2
A,Map position
A;Note: part of this sequence was confirmed by protein sequencing R;Fleming, J.C.; Pahl, H.L.; Gonzalez, D.A.; Smith, T.F.; Tenen, D.G. J. Immunol. 150, 480-490, 1993
A;Title: Structural analysis of the CD11b gene and phylogenetic analysis of the alpha-in n during evolution.
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                                                                                                                                              A, Reference number: A46526; MUID:93123748; PMID:8419480 A, Accession: A46526 A, Status: not compared with conceptual translation A, Molecule type: DNA
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R;Sastre, L.; Roman, J.M.; Teplow, D.B.; Dreyer, W.J.; Gee, C.E.; Larson, R.S.; Roberts, Proc. Natl. Acad. Sci. U.S.A. 83, 5644-5648, 1986
A;Title: A partial genomic DNA clone for the alpha subunit of the mouse complement receptainties: preliminary proposesion: 159078; MUID:86287312; PMID:2942940
A;Accession: 159078; MUID:86287312; PMID:2942940
A;Accession: 159078
A;Accession: 159078
A;Cross-reference: preliminary; translated from GB/EMBL/DDBJ
A;Cross-references: GB:M14293; NID:9198993; PIDN:AAA39484.1; PID:9554193
A;Gene: Mac-1
C;Genetics:
A;Gene: Mac-1
C;Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat home C;Keywords: cell adhesion; glycoprotein; transmembrane protein
F;1-16/Domain: signal sequence #status predicted <SIG.
F;17-1153/Product: leukcoyte surface glycoprotein Mac-1 alpha chain #status experimental F;148-3180/Domain: von Willebrand factor type A repeat home F;106.1194/Domain: von Willebrand factor type A repeat home F;106.1194/Domain: von Willebrand factor type A repeat home F;1106.1194/Domain: von Willebrand factor type A repeat home
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C.Species: Homo sapiens (man)
C.Species: Homo 1922 #sequence revision 31-Dec-1992 #text_change 09-Jul-2004
C.Accession: A.S6544, A.S5544
A.Soft and C.Species: A.Species: A.Speci
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GPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRL-ACESASSTE
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VRINOTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDI 1019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PVLRVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVT 660
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                                                                                                                                           121 FPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEWVSTVMEQLKKSKTLFSLMQYSEEF 180
                                                                                          RLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLRQQPQK 120
                                                                                                                  GLQVPPEAVNMSLGLSLASTTSPSQLLACGPTVHHECGRNMYLTGLCFLLGPT--QLTQR 137
                                                                                                                                                                  197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         721 SLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRTNKTEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        781 GPREFNVIVIVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEV
                                                                                                                                                                                                                                                     GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR
                                                                                                                                                                                                                                                                                                                                                                                              PRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRGWR-RWWCDAVLYGEQGHPWGRFGAALTVLGDVNGDKLTDVVIGAPGEEENRGAVYF
                                                                                                                                                                                          RIHFTFKEFQNNPNPRSLIKPITQLLGRTHTATGLRKVVRELFNITNGARKNAFKILFLL
                                                                                                                                                                                                      301 NFEALKTIQNQLREKIFAIEGTQTGSSSSFEHEMSQEGFSAAITSNGPLLSTVGSYDWAG
                                                                                                                                                                                                                                                                                                                                                                                  QNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPL
                                                                                                                                                         FNLDTEELTAFRVDSAGFGDSVVQYANSWVVVGAPQKITAANQTGGLYQCGYSTGACEPI
                                               FNLDTENAMTFOENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSTGSCEPI
                        Gaps
                       9
 Length 1163;
                        Indels
Query Match 59.0%; Score 3469; DB 1; Best Local Similarity 60.9%; Pred. No. 3.1e-233; Matches 688; Conservative 142; Mismatches 293;
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Alternate names: leukocyte adhesion glycoptotein LFA-1 alpha chain; leukocyte function of sulfare glycoprotein CD11a precursor - human N;Alternate names: leukocyte adhesion glycoptotein LFA-1 alpha chain; leukocyte function C;Species: Home sapiens (man) C;Accession: S03308; A47565; A48755; A87555;  A875555; A875555; A875555; A875555; A875555; A875555; A8755555; A8755555; A875555; A875555; A8755555; A875555; A875555; A875555; A875555; A875555; A875555; A875555; A8755555; A8755555; A8755555; A8755555; A8755555; A8755555; A875555; A875555; A8755555; A8755555; A8755555; A875555; A875555; A875555; A875555; A8755555; A8755555; A875555; A875555; A875555; A875555; A875555; A8755555; A875555; A875555; A875555; A875555; A875555; A875555; A8755555; A875555; A875555; A875555; A875555; A875555; A8755555; A8755555; A875555; A875555; A875555; A875555; A875555; A875555; A8755555; A875555; A875555; A875555; A8755555; A875555; A875555; A875555; A875555; A875555; A8755555; A8755555; A8755555; A8755555; A8755555; A8755555; A875555; A87
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A;Cross-references: CDB:11.2-16p11.2
C;Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat hom C;Keywords: cell adhesion; oylooprotein; heterodimer; surface antigen; tr F;1-25/Domain: signal sequence #status predicted <SIG>F;1-25/Domain: signal sequence #status predicted cSIG>F;26-1170/Product: leukocyte adhesion glycoprotein LFA-1 alpha chain #status predicted F;154-317/Domain: von Willebrand factor type A repeat homology <VWA2>
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                                                                                                                                      TKVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMMSF 1128
                                                                                                                                                                              Query Match 26.2%; Score 1543.5; DB 2; Best Local Similarity 34.3%; Pred. No. 6.2e-99; Matches 403; Conservative 210; Mismatches 460;
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LQGRPGFQECIKG----NVDLVFLFDGSMSLQPDEFQKILDFMKDVMKKLSNTSYQFAAV 196
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                                                                 HVFQINNFEALKTIONQLREKIFALEGTOTGSSSSFEHEMSQEGFSAAITSNGPLLSTVG 354
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                                                                                                                                                                                                                                 544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TSHNHLLIVSTABILFNDSVFTLLPGQGAFVRSQTBTKVEPFBVPNPLPLIVGSSVGGLL 1103
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                                                                                                                                                                                                                                                                                                                                                          EDPVSPIVLRINFSL---VGTPLS--AFGN-----LRPVLAEDAQRLFTALFPFEKNCGN 757
                                                                                                                                                                                                                                                                                                                                                                      DNICQDDLSITESFMSLDCLVVGGPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVS 817
                                                                                                                                                                                                                                                                                                                                                                                                            887
                  QYSEEFRIHFTFKEFQNNPNPRSLIKPITQLLGRTHTATGLRKYVRELFNITNGARKNAF
                                                      KILFLLTDGEKFGDPLGYEDVIPELDREGVIRYVIGVGDAFRSEKSRQELNTVASKPPRD
                             GAQGHVLLLRSQPVLRVKAIMEFNPREVARNVFECNDQVV-KGKEAGEVRVCLHVQKSTR
                                                                                                                               SYDWAGGVF-LYTSKEKSTFINMTRVDSDMNDAYLGYAAA-IILRNRVQSLVLGAPRYQH
                                                                                                                                             IGLVAMER--ONTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQT
                                                                                                                                                                                                        RGGQVSVCPLPRGQRARWQCDAV--LYGEQGPWGRFGAALTVLGDVNGDKLTDVALGAP
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lymphocyte fuction-associated molecule-1-alpha - mouse
(species: Mus musculus (house mouse)
(species: Mus musculus (house mouse)
(spacies: Musculus (house mouse)
(spacies: 26-dul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
(spaciession: 156126
3. Tamunol. 147, 369-374, 1991
3. Tamunol. 147, 369-374, 1991
3. Tamunol. 147, 369-374, 1991
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3. Tamunol. 156126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FQINNFEALKTIONQLREKIFALEGTQTGSSSSFEHEMSQEGFSAAITSNGPLLSTVGSY 356
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                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-1163 <RES>
A;Cross-references: UNIPROT:P24063; GB:M60778; NID:g198785; PIDN:AAA39426.1;
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Gene: LFA-1
C,Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type
F;151-315/Domain: von Willebrand factor type A repeat homology <VWAL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 IRLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLRQQPQ
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RESULT I56126

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integrin alpha-1 chain - human (fragment)
()Species: Homo sapiens (man)
()Species: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
()Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
()Accession: A45226
()Accession: A45226
()Accession: A5226
()Biol. Chem. 268, 2889-2996, 1993
()Thitle: Expression of native and truncated forms of the human integrin alpha 1 subunn
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|DERQVILGAVGAFDWSGGALLYDTRSRRGRFLNQTAAAAADAEAAQYSYLGYAVAVLHKT
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                                                                   SSPARS------GFLELMSSASLAVEWTLSNSGEDAYWVRLDLDFPRGLSFRKVEMLQ-
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Best Local Similarity 28.9%; Pred. No. 8.6e-71;
Matches 340; Conservative 214; Mismatches 451;
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A;Cross-references: GDB:330801
                                                 TESEMSIDCLVVGGP
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F; 199-371/Domain: von
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44; 106 388 ----SKTLFSLMOYSEEFRIHFTFKEFQNNPNPRSLIKPITQLLGR-THTATGLRKVV 219 349 SQTGFSAHYSQDWVMLGAVGAYDWNGTVVMQKASQIIIPRNTTFNVESTKKNBPL-ASYL 408 GYAAAIILRNRVQSL-VLGAPRYQHIGLVAMFRQNTGMWESNANVKGTQIGAYFGASLCS 447 VDVDSNGSTDLVLIGAPHY------YEQTR-GGQVSVCPLPRGQRARWQCD 491 AVLYGEQGOPWG-RFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLFHGTSGSGISP 550 SHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTVGAQGHVLLLRSQPVLRVKAIME 610 26 SCTTENKNEPCGARFGTALAAVKDINLDGFNDIVIGAPLEDDHGGAVYIYHG-SGKTIRK 587 ::||| EXAQRIPSGGDGKTLKFFGQSIHGEMDLNGDGLTDVTIGGLGGAALFWSRDVAVVXVTMN 647 FNPREVARNVFECNDQVVKGKEAG--EVRVCLHVQ-KSTRDRLREGQIQSVVTYDLALDS 667 PRE-FNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEV 840 GRPHSRAVENET-----KNSTRRQTQVLGLTQTCETLKLQLPNCIEDPYSPIVLRLNFS 721 LVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVGG 781 1 FNLDTENAMTFQENARG-FGQSVVQL---QGSRVVVGAPQEIVAANQRGSLYQCDYSTGS CEP-IRLOVPVEA-----VNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGL CSDVSPTFQVVNSIAP--VQECSTQ-LDIVIVLDGSNSIYPWDS-----VTAFLNDLLK RELFNITNGARKNAFKILFLLTDGEKFGDPLGYEDVIPELDREGVIRYVIGVGDAFR----CFLFGSNLRQQPQKFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEWVSTVMEQLKK --SEKSRQEINTVASKPPRDHVFQINNFEALKTIQNQLREKIFAIEGTQTGSSSSFEHEM 290 LSTEKFVEEIKSIASEPTEKHFFINVSDELALVTIVKTLGERIFALEATADQSAASFEMEM SQEGFSAAITSNGPLLSTVGSYDWAGGVFLYTSKE-----KSTF-INMTRVDSDMNDAYL RMDIGPKQTQVGIVQYGENVTHEFNLNKYSSTBEVLVAAKKIVQRGGRQTMTALGTDTAR LT-DPENG-----PVLDDSLPNSVHEYIPFAKDCGNKEKCISDLSLHVATTEKDLLIVRS 807 QNDKFNVSLTVKNTKDSAYNTRIIVHYSPNLVFSGIEAIQKD-----SCESN----A,Reference number: A45226; MUID:93155124; PMID:8428973
A;Accassion: A45226
A;Accassion: A45226
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-1151 <BRI>
A;Residues: 1-1151 <BRI>
A;Residues: 1-1151 ABRI>
A;Residues: 1-1151 ABRI>
A;Residues: 1-1151 ABRI>
A;Residues: 1-1151 ABRI>
A;Repernmental source: hepatoblastoma cell line HepG2
A;Roctimental source: hepatoblastoma cell line HepG2
A;Roctimental source: hepatoblastoma factor type A repeat homology <VWAI>
F;142-317/Domain: von Willebrand factor type A repeat homology <VWAI> 203; Query Match
18.6%; Score 1093.5; DB 2; Length
Best Local Similarity 27.8%; Pred. No. 1.5e-67;
Matches 345; Conservative 206; Mismatches 487; Indels 57 107 120 167 171 231 61 220 277 335 350 389 448 469 899 409 529 551 588 611 648 722 782 492 753 à g ð DP δ qq qq  $\dot{\delta}$ à Op ⋧ Op ð QQ ð 90 A9 B & B & Ωp 장염 ∂ à g ò

integri PID:943969 integrin alpha 2 subunit - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Abec: 16-Aug-1996 #sequence\_revision 16-Aug-1996 #text\_change 09-Jul-2004
C;Accession: 145914
R;Kamata, T: Puzon, W.; Takada, Y.
G;Boil: Chem. 269, 9659-9663, 1994
A;Title: Identification of putative ligand binding sites within the I-domain of if A;Reference number: A54402; MUID:94193647; PMID:7511592
A;Accession: 145914
A;Accession: 145914
A;Accession: I45914
A;Accessio ATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLPGQGAFVRSQTETKVEPFEVPN 1089 969 MPELKLSISFPNMTSNGYPVLYPTGLSS------SENANCRPHIFEDPFSINSGK 1017 -- OKRELAIQISKDGLPG 1110 47; FLFGSNLRQQPQKFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEWVSTVMEQLK-- 165 276 GSCEPIRLQ-----VPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLC 107 SDVSPDF-QLRISFAPAVQTCP-SFIDVVVVCDESNSIXPWD--AVKNFLEKFVQGLDIG 194 AYSTAAGGRPGATKVMVVVTDGESH-DGSKLKAVIDQCNKDNILRFFGIAVLGYLNRNALD 310 336 369 | EGFSAAIT--SNGPLLSTVGSYDWAGGVFLYTSKEKSTFINMT--RVDSDMN-DAYLGYA 391 78 221 54 ----HNITCKVGYPFLRRGEMVTFKILFQFNTSYLMENVTIYLSATSDSEEPPETLSDNV :::::| |::::::| XMTTSTD---HLKRGTILDCNTCKFATITCNLTSSDISQVNVSLILWKPTFIKSYFSSLN SGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGN-KLLLKANVTSENNMPRTNKTE 1 FNLDTENAMTFQ-ENARGFGQSVVQL---QGSRVVVGAPQEIVAANQRGSLYQC--DYST TTCEKLNLQTSTSMSNVTEMKTNMSLGLTLTRNVGTGGFLTCGPLWAQQCGSQYYTTGVC KSKTLFSLMQYSEEFRIHFTFKEFQNNPNPRSLIKPITQLL----GRTHTATGLRKVVRE PIKIQMGLIQYANNPRVVENLNTFKSKD---EMIKAISQTFQYGGDLINFKAIQYARDT SEKSRQELNIVASKPPRDHVFQINNFBALKTIQNQLREKIFAIBGTQTGSSSSFBHBMSQ Gaps Indels 168; ---LPISLVF-----LVPVRLNOTVIWDRPQVTFSENLSSTCHTKE Length 1170; LFNITNGARKNAFKILFLLTDGEKFGDPLGYEDVIPELDREGVIRYVIGV-900 FQLELPVKYAVYMVVTSHGVSTKYLNFTASENTSRVMQHQYQVSN-PLPL--IVGSSVGGLLLLALITAALYKLGFFKRQYKDMMSE 1128 RLPSHSDFLAELRKAPVVNCSIAVCORIQCDIPFFGIQE---18.2%; Score 1071; DB 2; Similarity 27.4%; Pred. No. 5.5e-66; 13; Conservative 219; Mismatches 495; LTIRGEL-----RSENASLVLSSSN--Query Match Best Local Simil Matches 333; C 1018 1030 1075 1090 854 988 19 79 108 139 166 195 222 252 277 337 RESULT 145914 q δ g à d à g  $\dot{\delta}$ Dp  $\stackrel{>}{\circ}$ qq à g à d g ò ŏ dd à g ò 유 à

| OY TANDERS OF THE PROPERTY OF  |  | Query Match<br>Best Local Similarity 27.8%; |
|--|--|---|
| 430  |  | ches 340;                                   |
| Qy 446 CSVDVDSNGSTDLVIJGAPHYYEQTRGGQVSVCFLPRGORARWQCDAVLYGEQGGPWG  | 503  |   |
|  | DD   | D 27 YNVGLPGAKIFSGPSSEQFG                   |
| OY 504 KEGAMILY DO NO DALIO NO | 009  |   |
| 239  | 621  | Db 87 ATCEKLNLQNSASISNVIEI                  |
| HINDS  |  | 108   |
| TINTES TOP   | SGRPHSRAVEN 677  | Db 147SDVSPDFQFLTSFSPA                      |
| OY OZZ BCNDOV VNGKBAGBYN CLINY GALLIADALIAN  | OFSERVISEGIFK 707  | OY 165 KKSKTLFSLMQYSBEFRI                   |
| OD STANDARD CONTRACTOR OF THE STANDARD CONTRACTO | 733  | Db 200 DIGPKKTQVALIQYANEPR                  |
| 8/9  | 930  | Qy 222 LENITNGARKNAFKILFLLT                 |
| Db 708 ENNERCLOKTMIVSQAQRCSEYIIHIQEPS-   | 007  | Db 260 AYSQTSGGRPGATKVMVVT                  |
|  | 789  | Qy 277 SEKSRQELNTVASKPPRDHV                 |
| Db 757 NPALEAYSETVKVFSIPFHKDCGDDGVCISI   | QTP  | Db 319 TKNLIKEIKAIASTPTERYF                 |
| Qy 790 TVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASST-EVSGALKSTS Qy ::    :  :   :  :   :  :  :  :  :  :  :   | 848  | Oy 337 EGFSAAITSNGPLLSTVG                   |
| Db 817 QLKNKKĖSAYNTEIVVDĖSENLFF  | 864  | Db 378 VGFSADYAPQNDILMLGAVG                 |
| Qy 849 CSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRTNKTEFQLELPVKY   :     :     :     :     :     :     :  | 808  | Qy 392 AAIILRNRVQSLVLGAPRYÇ                 |
| Db 865 CNVGYPALKSKQQVTFTINFDFNLQ-NLQNC   | 923  | Db 438 VAAISTEDGVHFVAGAPRAN                 |
| QY 909 AVYMVUTSHGVSTKYLNFTASENTSRVMQHQYQVSNLGQR-   | V 958  | Qy 448 VDVDSNGSTDLVLIGAPHYY                 |
| Db 924 DAEIHIT-RSTNINFYEVSLDGNVSSVV-HSFEDIGPKFIFSIKVTTGSVPVSMA   | - 976  | :     :                                     |
| QY 959 PVRINQTVIMDRPQVIFSENLSSTCHTKE   |  | Qy 506 GAALTVLGDVNGDKLTDVAI                 |
| Db 977SVİIHIPQYTKDKNPLMYLTGVHTI  | -SVIIHIPQYTKDKNPLMYLTGVHTDQAGDISCEAEINPLKIGQTSSSVSFKSEN 1030 | Db 552 GSAIAALSDINMDGFNDVIV                 |
| Qy 999 LRKAPVVNCSIAVCQRIQCDIPFFGIQEBFNATLKGNLSFDWYIKTSHNHLLIVSTAEI   | 1057   | Vy 565 -LQXFGQSLSGGQDLTMDGI                 |
| Db 1031 FRHIKELNCRTASCSNIMCWERDLQVKGEYFLNVSTRIWNGTFAASTFQTVQLTAAAEID   | 1090   | :   |
| Qy 1058 LFNDSVFTLLPGQGAFVRSQTETK   | 1110   | Qy 624 NDQVVKGKEAGEVRVCLHVQ                 |
| Db 1091 TYNPQIYVIEENTVTIPLTII  | -LTIMKPHEKVEVPTGVIVGSVIAĞILLILALVA 1140                      | Db 661 -DKITLINKDAKITLKICF                  |
| Qy 1111 ALYKLGFFKRQYKDM 1125   |  | Qy 680 KNSTRRQTQVLGLTQTCET                  |
| Db 1141 ILWKLGFFKRKYEKM 1155   |  | Db 718 SERFLOKNWVNEVOKCSE                   |
| RESULT 9   |  | Qy 738 AEDAQRLFTALFPEKNCG                   |
| S44142<br>VLA-2 protein homolog - mouse  |  | Db 769 EAYSETVKVFSIPFYKECG                  |
| C;Species: Mus musculus (nouse mouse)<br>C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995  | ext_change 09-Jul-2004                                       | QY 789 VIVRNDGEDSXRIQVIFFF                  |
| C,Accession: S44142<br>R;Edelman, J.M.; Chan, B.M.; Uniyal, S.; Ono  | Wang, D.Z.; Damjanovich, L.; Latze                           | Db 824 VILKNRGESAYNTVVLAEF                  |
| submitted to the EMBL Data Library, January 1594 A, Description: The mouse VLA-2 homologue supports col  | lagen and laminin adhesion but not                           | Qy 848 SCSINHPIFPENSEUTFNI'                 |
| A; Kererence number: 544142<br>A; Accession: 544142  |  | Db 872 TCDVGYPALKSBQQVTFTI                  |
| A;Status: preliminary<br>A;Molecule type: mRNA   |  | Qy 906 VKYAVYMVVTSHGVSTKYL                  |

9; EMBL:229987; NID:9473098; PIDN:CAA82877.1; PID:9473 factor type A repeat homology <VWA2> 905 FSENLFF------ASFSMPVDGTEVTCEVGSSQKSV 871 | || : : : | | : : | | : : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | | : | : | | : | : | | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : --SLPISLV 955 | |:|: GNDNICQDDLSI-----TFSFMSLDCLVVGGPREFNVT 788 44; GLVDLTVGAQGHVLLLRSQPVLRVKAIMEFNPREVARNVFEC 623 VOKSTRDRLREGOIQSVVTYDLALD----SGRPHSRAVFNET 679 T--LKLOLPNCIEDPVSPIVLRLNFSLVGTPLSAFGNLRPVL 737 IVFQINNFEALKTIQNQLREKIFALEGTQTGSSSSFEHEMSQ 336 377 VGSYDWAGGVFLYTSKEKSTFINMT--RVDSDMN-DAYLGYA 391 437 447 505 YMNDLKKEEGKVYLFTITKGILNQHQ---FLEGPEGTGNARF 551 564 EAVNMSIGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLC 107 ALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEWVSTVMEQL 164 LHFTFKEFONNPNPRSLIKPITQLLG-RTHTATGLRKVVRE 221 54 98 FPLDLSYRKVSTLQNQRSQRSWRLACESASST-EVSGALKST ITEDVDSKASLGNKLLLKANVTSENNMPRTNKTE--FOLELP YYEQTR--GGQVSVCPLPRGQRARWQCDAVLYGEQGQPWGRF 1 I FNI, ND FETKED MVQATSETROHGGDLTNTFRAIEFARDY YQHIĞLVAMFRQNTGMWESNANV----KGTQIGAYFGASLÇŞ AIGAPGEEDNRGAVYLFHGTSGSGISPSHSORIAGSKLSPR-GOSVVQL---QGSRVVVGAPQEIVAANQRGSLYQC--DYST Gaps Indels 188; Length 1178; LNFTASENTSRVMQHQYQVSNLGQR---Score 1057; DB 2; I Pred. No. 5.3e-65; .0; Mismatches 487;

us-09-902-481b-4.rpr

| 448 VDVDSNGSTDLVLIGAPHYYEQTR-GGQVSVCPLPRGQRARWQCD 491                         |   | OY 940 YQVSNLGQRSLPISLVFLVPVRLNQTVIWD   | RESULT 11 A33998 integrin alpha-2 chain precursor - human N;Alternate names: CD49b; platelet glycoprotein GPIa; VLA-2/collagen receptor alpha-2 c C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 30-Mar-1990 #sequence_revision 18-Sep-1992 #text_change 09-Jul-2004 C;Date: 30-Mar-1990 #sequence_revision 18-Sep-1992 #text_change 09-Jul-2004 R;Takada, Y; Hemler M.E. U; Cell Biol. 109; 339-407, 1989 A;Title: The primary structure of the VLA-2/collagen receptor alpha(2)-subunit (platelet A;Reference number: A33998; MuID:89308879; PMID:2545729 A;Reference number: A33998; MuID:89308879; PMID:2545729 A;Robecule type: mRNA A;Residues: 1-1181 < TARx> A;Residues: 1-1181 < TARx> A;Cross-references: UNIPROT:P17301; GB:X17033; NID:g33906; PIDN:CAA34894.1; PID:g33907 A;Note: the authors translated the codon GAT for residue 802 as Gln, GTC for residue 803 |
|---|---|---|--|
| Db 929 LLYDAELHLT-RSTNINFYEISSDENAPSVIKSVEDIGPKFIFSLKVTAGSAFVSMA 984  956 FLV | RESULT 10 A35854 integrin alpha-1 chain precursor - rat C;Species: Rattus norvegicus (Norway rat) C;Species: Rattus norvegicus (Norway rat) C;Date: 23-Oct-1990 #sequence_revision 13-Sep-1991 #text_change 09-Jul-2004 C;Accession: A35864; S11243 R;Ignatius, M.J.; Large, T.H.; Houde, M.; Tawil, J.W.; Barton, A.; Esch, F.; Carbonetto. J. Call Biol. 111, 709-720, 1990 A;Title: Molecular cloning of the rat integrin alpha-1-subunit: a receptor for laminin and A;Reference number: A35854; MUID:90338125; PMID:2380249 A;Reference number: A35854 A;Redaus: preliminary A;Molecule type: mRNA A;Residues: 1-180 cdns A;Residues: 1-180 cdns C;Keywords: cell adhosion; Cytoskeleton; transmembrane protein C;Keywords: cell adhosion; Cytoskeleton; transmembrane protein F;170-345/Domain: von Willebrand factor type A repeat homology cVWA2> | Query Match         17.9%; Score 1055; DB 2; Length 1180;           Best Local Similarity 27.4%; Pred. No. 7.3e-65;         Adches 346; Conservative 196; Mismatches 475; Indels 246; Gaps 48;           QY         1 FNLDTENAMTFQENARG-FCQSVVQLQGSRVVVGAPQEIVAANQRGSLVQCDXSTGS 56           Db         29 FNVDVKNSMSFSGPVEDMFGYTVQQYENEEGKWVLIGSPLVGQPRARTGDVYKCPVGRER 88           QY         57 CEP-IRLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGL 106           Db         89 AMPCVKLDLPVNTSIRENWTFGSTL-VTNPNGGFLACGPLXAYRCGHLHYTTGI 147           QY         107 CFLFGSNLRQQPQKFPEALRGCPGDSDIAFLIDGSGSIIPHDFRRMKEWVSTVMEQ 163           Db         148 CSDVSPTFQVVNSFAPVQECSTQ-LDIVIVLDGSNSIRYP |  |

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murine lymphocyt
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624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YNLDPENALLYQGPSGTLFGYSVVLHSHGSKRWLIVGAPTASWLSNASVVNPGAIYRCGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LPSHSDFLAELRKAPVVNCSIAVCQRIQCDIPFFGIQEEFNATLKGNLSFDWYIKTSHNH
                                                                                                                                                               AYSETAKVPSIPPHKDCGEDGLCISDLVLDVRQIPAAOEOPFIVSNONKRLIPSVTLKNK
                                                                                                                                                                                                                                                                                   795 GEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASST-EVSGALKSTSCSINH
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----LNCRTASCSNVTCWLKDVHMKGEYFVNVTTRIWNGTFASSTFQT
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                                                                                          EDAQRIFTALFPEKNCGNDNICQDDLSITF----SFMSLDCLVVGGPREFNVTVTVRND
                                                                                                                                                                                                                                                                                                                                                        PI FPENSEVTENI TFDVDSKASLGNKLLLKANVTSENNMPRTNKTEFQLEL PVKYAVYMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----PVRLNOTVIWDRPQVTF-SENLSSTCHTKER
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                                                                                                                                                                                                                                                                                                                       ----ASFSLPVDGTEVTCQVAASQKSVACDVGX
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                        LQYFGRSLDGYGDLNGDSITDVSIGAFGQVVQLWSQSIADVAIBASFTPEKI--TLVNKN
                                                                                                                                          NSTRRQTQVLGLTQTC--ETLKLQLPNCIEDPVSPIVLRLNFSLVGTPLSAFGNLRPVLA
                                                                                                                                                                                                                                                                                                                                                                                                                              ---SLPISLVFLV---
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.larity 22.7%; Pred. No. 1.3e-37;
Conservative 187; Mismatches 403; Indels 368;
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                                                                        DOVVKGKEAGEVRVCLHVOKSTRDRLREGQIQSVVTYDLALD-
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A,Molecule type: mRNA
A,Residues: 1-1039 (NEDA)
CYCOSS-references: UNIPROT:Q00651; EMBL:X53176;
C,Superfamily: integrin alpha-4 chain
C;Keywords: cytoskeleton; transmembrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SADYSSONDILMLGAVGAFGWSGTIVQKTSHGHLIFPKQAFDQILQDRNHSSYLGYSVAA 443
                                                                                                                                                                                                                                                                                                                 C;Genetics: GBS:17GA2; CD49B
A;Gene: GBB:17E8031; OMIM:192974
A;Gene: GBB:17E8031; OMIM:192974
A;Gene: GBB:17E8031; OMIM:192974
A;Map Position: Sq11.1-5q11.2
C;Keywords: cell adhesion; glycoprotein; heterodimer; transmembrane protein C;Keywords: cell adhesion; glycoprotein; heterodimer; transmembrane protein E;1.29/Domain: extracellular #status predicted <EXT>
F;10-1133/Domain: von Willebrand factor type A repeat homology <VWA2>
F;1172-347/Domain: transmembrane #status predicted <TWM>
F;1115-1181/Domain: intracellular #status predicted <CYT>
F;105,112,343,432,460,475,699,1057,1074,1081/Binding site: carbohydrate (Asn)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DVDSNGSTDLVLIGAPHYYEQTR--GGQVSVCPLPRGQRARWQCDAVLYGEQGQPWGRFG
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Best Local Similarity 26.7%; Pred. No. 8.6e-65;
Matches 327; Conservative 216; Mismatches 494; Indels 188;
         R;Carimel, B.; Parmentier, S.; Leung, L.L.; McGregor, J.L. Biochem. J. 279, 419-425, 1991
A;Title: Separation of important new platelet glycoproteins A;Reference number: A56793; WUID:92061944; PMID:1953640
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ENVAHVFLEGLHHQRPKRHF 983
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                                                                                                                          ain; VLA-4 alpha chain
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248 445 505

364

308

423 623 482 531 728 591 777 647 837 701

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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residues: 1-1035 -RES>
A;Cross-references: UNIPROT:Q13797; GB:D25303; NID:9464180; PIDN:BAA04984.1; PID:953332
A;Cross-references: UniPROT:Q13797; GB:D25303; NID:9464180; PIDN:BAA04984.1; PID:953332
B;Palmerr E.L.; Ruegg; C.; Ferrando, R.; Pytela, R.; Sheppard, D.
J. Cell Biol. 123, 1289-1297, 1993
A;Pitle: Sequence and tissue distribution of the integrin alpha9 subunit, a novel partn A;Reference number: A49459; MUID:94064789; PMID:8245132
A;Accession: A49459
A;Accession: A49459
A;Accession: A49459
A;Accession: A49459
A;Cross-references: GB:L24158
A;Residues: 30-1035 cPAL>
A;Cross-references: GB:L24158
A;Cross-references: GB:L24158
C;Superfamily: integrin alpha-4 chain
C;Keywords: glycoprotein; metal binding; transmembrane protein
C;Keywords: glycoprotein; metal binding; transmembrane protein
F;1-27/Domain: signal sequence #status predicted <516>
                                                                                                                                                                                                                                                                                                                                                                                            EHEMSQEGFSAAITSNGPLLSTVGSYDWAGGVFLYTSKEKSTFINMT-RVDSDMNDAYLG 389
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                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                          10.7%; Score 630; DB 2; 26.5%; Pred. No. 2.6e-35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1026 EEFNATLKGNLSFDWYIKTSHNHLLIVSTAE----ILFN-----DSVFTLLPGQG 1071
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                                       LLSTVGSYDWAGGVFLY---TSKEKSTFINMTRVDSDMNDAYLGYA--AAIILRNRVQSL
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|---|--|---|-----|---|--|---|---|--|--|--|---|--|
| QY 1040 WYIKTSHNHLLIVSTREILENDSVFTLLPGQGAFVRSQTETKVEP | A,Description: binds laminin<br>C,Superfamily: integrin alpha-2b chain | Query Match<br>Best Local Similarity 24.8%; Pred. No. 3.1e-34;<br>Matches 236; Conservative 155; Mismatches 314; Indels 245; Gaps 41; | 336 | QY 390 YAAAIILRNRVQSLVLGAPRYQHI-GLVAMFRQNTGMWESNANVKGTQIGAYFGASLC 446 | QY 447 SVDVDSNGSTDLVLIGAPHYYEQIRGGOVSVCPLPRGGRARWQCDAVLYGEQ 498      :   :   :   : | QY 499GQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNRCAVYLFHGTSGS 546  Db 344 SNRLSLSSTLIGGQIRSRFGLSIASIGDSNQDGPNDVAIGAPYEGDDAGAVYIYHG-SAN 402 | QY 547 GISPSHSQRIAGSKLS-PRLQYPGQSLSGGQDLTMDGLVDLTVGAQGHVLLLRSQPVL 603 | OY 604 RVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRDRLREGGIQSV 658 | QY 659VTYDLALDSG-RPHSRAVENETRNSTRRQTQVLGL-TQTCETLKLQ 702 | QY 703 LPNCIEDPVSPIVLRLNFSLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEK 753 | QY 754 NCGNDNICQDDLSITFSFMSLDCLVVGGPREFNVTVTVRNDGEDSYRTQVFFFFPLDLSY 813 | QY 814 RKVSTLQNQRSQRSWRLACESASSTEVSGALKSTSCSINHPIFPENSEVTFNIT 867  ::::::: |

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GenCore version 5.1.6
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OM protein - protein search, using sw model

November 9, 2004, 11:46:42; Search time 136.75 Seconds (without alignments) 4783.919 Million cell updates/sec Run on:

US-09-902-481B-4 5884 1 FNLDTENAMTFQENARGFGQ......FKRQYKDMMSEGGPFGAEFQ 1137 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1825181 seqs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt\_02:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARIES

| Description                | 11121 CMCH 21121 |            |                 |        |            | homo       | mus m  |          | Q9qxh4 mus musculu |          |            |            | bos t  | 15 bc    | P24063 mis miscilii | Sim    | MUS.   |        |        |        |        | ratt   | _          | 0 homo     | rattu  | -          | O WOO      | Post<br>1  | 2 2        | 300    | 39 mu    |
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| SUMMARIES                  | ITAM HUMAN       | ITAM MOUSE | 09JI <u>3</u> 0 | 028984 | ITAX HUMAN | ITAD HUMAN | Q6KAS4 | BAD21383 | ITAX MOUSE         | ITAD_RAT | ITAL_BOVIN | ITAL_HUMAN | Q6TYB8 | AAQ90015 | ITAL MOUSE          | Q9WTV4 | Q9R200 | 098TF1 | 096нв1 | OSSTFO | Q8HZV0 | 088340 | ITAE MOUSE | ITAE HUMAN | 088341 | ITA1 HUMAN | ITAH HUMAN | ITA2 BOVIN | ITA2 MOUSE | Q6P1C7 | AAH65139 |
| DB                         | : <del>.</del>   | Н          | 7               | N      | Н          | Н          | 7      | ~        | Н                  | -        | ٦          | -4         | 7      | N        | Н                   | 7      | 7      | ~      | 7      | ~      | 7      | 7      | Н          | Н          | 7      | Н          | ٦          | Н          | Н          | ~      | 01       |
| %<br>Query<br>Match Length | 1152             | 1153       | 1151            | 920    | 16         | 1162       | 1188   | 1188     | 1169               | 1161     | 1165       | 1170       | 1166   | 1166     | 1163                | 1161   | 1160   | 1196   | 1086   | 1187   | 927    | 1167   | 1167       | 1179       | 1167   | 1151       | 1189       | 1170       | 1178       | 1178   | 1178     |
| %<br>Query<br>Match        | 99.2             |            |                 |        |            | 57.8       | 56.4   | 56.4     | 56.3               | 55.0     |            |            |        |          |                     | 25.9   |        |        | 23.0   |        |        |        |            | 6          |        | •          |            | •          | 18.0       | 18.0   | 18.0     |
| Score                      | ന                | 4460       | 4371            | 3799.5 | 3469       | 3401       | 3319.5 | 3319.5   | 3310.5             | 3236.5   | 1572       | 1547.5     | 1546   | 1546     | 1527.5              | 1523.5 | 1513   | 1395   | 1350.5 | 1344.5 | 1269   | 1154.5 | 1148.5     | 1140       | 1109   | 1093.5     | 1084.5     | 1071       | 1057       | 1057   | 1057     |
| Result<br>No.              | Н                | 7          | c               | 4      | Ŋ,         | 91         |        | œ (      | ט נ                | o i      | 11         | 77         | 13     | 14       | 15                  | 16     | 17     | 18     | 19     | 20     | 21     | 22     | 23         | 24         | 52     | 56         | 27         | 28         | 29         | 30     | 31       |

| P18614 rattus norv<br>P17301 homo sapien<br>O75278 homo sapien<br>P61622 mus musculu<br>O42094 gallulus gall<br>O8b801 mus musculu<br>O9wuf8 mus sp. itg<br>Q8mKf felis silve<br>Q8mKf felis silve<br>Q8mS halocynthia<br>Q63001 rattus norv<br>Q6pg66 mus musculu<br>Aah57200 mus muscul |
|---|
| ITA1_RAT<br>ITA2_HUMAN<br>ITAA_HUMAN<br>ITAH_MOUSE<br>Q7TQG3<br>Q8TS01<br>Q9WUF8<br>Q8MXF4<br>Q8MXF4<br>Q8MXF4<br>Q8TES5<br>Q9TES5<br>Q6FQG6<br>AAH57200  |
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| 11181<br>1167<br>11188<br>11188<br>11171<br>1038<br>1160<br>348<br>1332<br>205<br>205<br>304  |
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## ALIGNMENTS

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S52153;
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S52155;
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S52159;
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S52165;
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M76724;
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granulocytes.

DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins a SIMILARITY: Belongs to the integrin alpha chain family.

SIMILARITY: Contains 7 FG-GAP repeats.

SIMILARITY: Contains 1 VWFA domain.

DATABASE: NAME-PROW; NOTE-CD guide CD11b entry;

WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd11b.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 17-31.
MEDLINE=87076671; PubMed=3539202;
Pierce M.W., Remold-O'Donnell E., Todd R.F. III, Arnaout M.A.;
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W.-terminal sequence of human leukocyte glycoprotein Mol: conservation across species and homology to platelet IIb/IIIa.";
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                                                                                                                                                                                                                                                                                                                      Lee J.O., Bankston L.A., Arnaout M.A., Liddington R.C.; "Two conformations of the integrin A-domain (I-domain): a pathway for
                                                                                                                                                                                                                                                                                                                                                                  **RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 148-337.

**MEDLINE=98362595; PubMed=9687375;

Baldwin E.T., Sarver R.W., Bryant G.L. Jr., Curry K.A.,

Fairbanks M.B., Finzel B.C., Garlick R.L., Heinrikson R.L.,

**Mutchler V.T., Tomich C.S., Matenpaugh K.D., Wiley V.H.;

"Catton binding to the integrin CDllb I domain and activation model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-Massociates with beta-2. SUBCELLULAR LOCATION: Type I membrane protein. TISSUE SPECIFICITY: Predominantly expressed in monocytes and
                    SEQUENCE OF 1-9 FROM N.A.
MEDLINE=92073318; PubMed=1683702;
Shelley C.S., Arnaout M.A.,
"The promoter of the CD11b gene directs myeloid-specific and developmentally regulated expression.";
Proc. Natl. Acad. Sci. U.S.A. 88:10525-10529(1991).
                                                                                                              MEDLINE=92144986; PubMed=1346576;
Pabll H.L., Rosmarin A.G., Tenen D.G.; "Characterization of the myeloid-specific CD11b promoter.";
Blood 79:865-870(1992).
                                                                                                                                                                                                                                                                                                  CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 148-334.
                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 148-331.
MEDLINE=95171458; PubMed=7867070;
  Proc. Natl. Acad. Sci. U.S.A. 86:257-261(1989).
                                                                                                                                                                                                                                                                                            [10]
X-RAY CRYSTALLOGRAPHY (2.0 ANGSTRC
MEDLINE=96363671; PubMed=8747460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fibrinogen gamma chain.
                                                                                                                                                                                                                                                                                                                                                     Structure 3:1333-1340(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                              assessment.";
Structure 6:923-935(1998).
                                                                                          SEQUENCE OF 1-9 FROM N.A.
                                                                                                                                                                                                                                                                                  Cell 80:631-638(1995).
                                                                                                      TISSUE=Blood;
                                                                                                                                                                                                                                                                                                                                            activation?"
                [9]
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                         modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PRINTS; PRO1453; VWFADOMAIN.
SMART; SMO0191; Int_alpha; 5.
SMART; SMO0192; VWFA, 1.
PROSITE; PSO0242; INTEGRIN_ALPHA; 1.
PROSITE; PSO0244; VWFA; 1.
3D-structure; Calcium, Cell adhesion, Direct protein sequencing; Glycoprotein; Integrin; Magnesium; Receptor; Repeat; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO: GO:0008305; C:integrin complex; GO: GO:0007155; P:cell adhesion; TAS InterPro; IPR000413; Integrin_alpha.InterPro; IPR002035; WWF_A.
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Pfam; PF00357; Integrin_alpha; 1.
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PDB, 11A8X; Model, G=17-1152.
PDB, 1BHO; X-ray, 1/2=-
PDB, 1BHO; X-ray, 1/2=-
PDB, 1IDN; X-ray; 1/2=-
PDB, 1IDN; X-ray; 6=140-331.
PDB, 1IDO; X-ray; G=140-331.
PDB, 1MU; X-ray; G=143-334.
PDB, 1MIU; X-ray; A=144-337.
PDB, 1MF7; X-ray; A=144-335.
PDB, 1N9Z; X-ray; A=140-335.
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EMBL; M18044; AAA59491.1; -.
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AAB24821.1;
AAB24821.1;
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| Db 976 RLNQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDIP 1035  Qy 1021 FFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLPGQGAFVRSQTET 1080  Db 1036 FFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLPGQGAFVRSQTET 1095 | QY         1081 KVEPFEVPNPLPLIVGSSVGGLLLALITAALYKLGFFKRQYKDMMSEGGPPGAEPQ 1137           Db  | SULT 2<br>AM_MOUSE<br>_ITAM_MOU  | P0555; QBCA73;<br>01-NOV-1988 (Rel. 09, Creat<br>01-FEB-1991 (Rel. 17, Last<br>05-JUL-2004 (Rel. 44, Last | DE Integrin alpha M precursor (Cell surface glycoprotein MAC-1 alpha DE subunit) (CR-3 alpha chain) (CD11b) (Leukocyte adhesion receptor MO1).  GN Name=Itgan, OS Mus musculins (Monse) |          |      | RT with the integrin family and an additional domain reveals homology RT with the integrin family and an additional domain related to von RL Willebrand factor."; RL EMPO J. 7:1371-1378(1988). | RP SEQUENCE FROM N.A. (ISOFORM 2).  RC STRAIN-C57BL/6J; IISSUB=Spinal cord;  RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  RA OKRAZAK! Y. FINTHO M PARTHEWS TO ARRANGE TO THE TOTAL TO | RA Nikaido I., Osato N., Salto R., Yanachi U., Boho H., Kohoo S., RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., RA Baldaralli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., RA Schrim I. W. Kananin N. Marmada I. M. Mananin N. Mananin N. Marmada I. M. Mananin N. Marmada I. M. Mananin N. Marmada I. M. Mananin N. Mananin N. Mananin N. Marmada I. M. Mananin N. Ma | RA Blake J.A., Bradt D., Brusic W., Couchia C., Corbani L.B., Cousins S., RA Dalla B., Dragani T.A., Fletcher C.F., Forcest A., Frazer K.S., RA Gasterfland T., Gariboldi M., Gissi C., Godzik A., Gough J., RA Grimmond C. Guerincick C. Historia | RA Kanai A., Kawaji H., Kawasawa Y., Kaczierski R.M., King B.L., RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., RA Maglott D.R., Martais L., Marchionni L., McKenzie L., Miki H., RA Nagashima T. Nimara K. Orido Trons. | RA Petrovsky N., Pillai R., Pontius J.U., Oi D., Ramachandran S., Ravasi T., Reed J.C., Reed D.J., Reid J., Ramachandran S., RA, Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., RA Sultana R. Takonaka V. Tanaka V. Takonaka V. | RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watenabe Y., Wells C., RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L., Yang J., Rah Hirozane-Kishikawa T. Komo, H. Carningi P., Hayatsu N., RA Hirozane-Kishikawa T. Komo, H. | Shiraki T., Waki K., Kawai J., Alzawa K., Arakawa T. Bukuda Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yashino M. Wararata D., Shibata K., Shinagawa A., Yashino M. | RA Birney E., Hayashizaki Y.; RT "Analysis of the mouse transcriptome based on functional annotation of RT 60,770 full-length CDNAs."; RL Nature 420:563-573 (2002). | [3] SEQUENCE OF 11-45 FROM N.A. STRAIN-BALB/C; TISSUE=Spleen; MEDLINE=86297312; PubMed=2942940; Saftre I. Pomen I M. |   |
|--|---|--|---|---|----------|------|---|--|--|--|---|--|---|---|--|--|---|
| FT SIGNAL 1 16 Integrin alpha-M.  Query Match 99.2%; Score 5836.5; DB 1; Length 1152;  Best Local Similarity 99.1%; Pred: No.0;  Matches 1127; Conservative 7; Mismatches 2; Indels 1; Gaps 1;                                 | Oy 1 FNLDTENAMTFOENARGFGOSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSTGSCEPI 60  Db 17 FNLDTENAMTFQENARGFGOSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSTGSCEPI 76 | OY 61 RLOVPVEANNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLRQQPQK 120 | Oy 121 FPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEWVSTVMEQLKKSKTLFSLMQYSEEF 180                                   | OY 181 RIHFTEKEFONNPNPRSLIKPITOLLGRTHTATGLRKVVRELFNITNGARKNAFKILFLL 240  Db 197 RIHFTEKEFONNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVI 256  | FOIN<br> | OWAG | GAPRYQHIGLVAMFR   | OY 421 QNTGMMESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPL 480  | QY 481 PRGQRARWQCDAVLYGEQGQPWGRPGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLF 540 DD 497 PRG-RARWQCDAVLYGEQGQPWGRPGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLF 555  | CTVGAQGHVLLLRSQ<br>            <br>LTVGAQGHVLLLRSQ   | Oy 601 PVLRVKAIMEENPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRDRLREGQ1QSVVT 660<br>DD 616 PVLRVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRDRLREGQ1QSVVT 675  | 661 YDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNF 720<br>   | 721 SLVGTPLSAFGNLRPVLAEDAQRLFTALFPFERNCGNDNICQDDLSITFSFMSLDCLVVG 780<br>  | rev<br>   | 841 SGALKSTSCSINHPIPPENSEVTENIFFDVDSKASLGNKLLLKANVTSENNMPRINKTEF 900<br>   | 01   | 961 KLNOTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDIP 1020 |

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Proc. Natl. Acad. Sci.
                                         .gnal; Transmembrane
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                                                                                            Springer T.A., Teplow D.B., Dreyer W.J.;

Springer T.A., Teplow D.B., Dreyer W.J.;

"Sequence homology of the LPA-1 and Mac-1 leukocyte adhesion

"Sequence homology of the LPA-1 and Mac-1 leukocyte adhesion

"I springer Integrin alpha-W/beta-2 is implicated in various

as well as in mediating the uptake of complement-coated particles.

It is identical with CR-3, the receptor for the iC3b fragment of the third complement component. It probably recognizes the R-G-D peptide in C3b. Integrin alpha-W/beta-2 is also a receptor for fibrinogen, factor X and ICAM1. It recognizes P1 and P2 peptides

of fibrinogen gamma chain. Alpha-W/beta-2 play a critical role in mast cell development and in immune complex-mediated

glomerationephritis. Mice expressing a null mutation of the alpha-M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              granulocytes.
-!- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins with I-domains do not undergo protease cleavage.
-!- SIMILARITY: Belongs to the integrin alpha chain family.
-!- SIMILARITY: Contains 7 FG-GAP repeats.
                                                                                                                                                                                                                                                                                                                                                                     subunit gene demonstrate increase in neutrophil accumulation, in response to a impaired degranulation and phagocytosis, events that apparently accelerate apoptosis in neutrophils. These mice develop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct protein sequencing; Glycoprotein; Integrin; Receptor; Repeat;
    type 3 and cellular adhesion molecule Mac-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=P05555-2; Sequence=VSP_010473;
Note=No experimental confirmation available;
-!- TISSUE SPECIFICITY: Predominantly expressed in monocytes and
                                                                                                                                                                                                                                                                                                                                                                                                                                        obesity.
SUBUNIT: Heterodimer of an alpha and a beta chain. Alpha-M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X07640; CAA30479.1; -.

EMBL; AK039444; BAC20350.1; -.

EMBL; MAC931, AA39484.1; -.

EMBL; MAC931, S00551.

HSSP, P11215; 1BHQ.

MGD; MGD; MGD; Tesam.

GO; GO:0009897; C:external side of plasma membrane; IDA.

GO; GO:0009897; C:external side of plasma membrane; IDA.

GO; GO:0009897; C:external side of plasma membrane; IDA.

GO; GO:0009897; P:cellular extravasation; IMP.

GO; GO:0030593; P:neutrophil chemotaxis; IMP.

InterPro; IPR002035; VWF.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          associates with beta-2.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alternative splicing; Calcium; Cell adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=P05555-1; Sequence=Displayed;
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PROSITE; PS50234; VWFA; 1.
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Pfam; PF000357; Integrin alpha; 1.
Pfam; PF00092; VMA; 1.
PRINTS; PR00185; INTEGRINA.
PRINTS; PR00453; VWFADOMAIN.
SWART; SM00191; Int_alpha; 5.
SWART; SM00191; Int_alpha; 5.
                                                                  SEQUENCE OF 17-28.
MEDLINE=85188276; PubMed=3887182;
            complement receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 FPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEWVSTVMEQLKKSKTLFSLMQYSEEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 IDGEKEGDPLGYEDVIPELDREGVIRYVIGVGDAFRSEKSROELNTVASKPPRDHVFOIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 FNLDTEHPMTFQENAKGFGQNVVQLGGTSVVVAAPQEAKAVNQTGALYQCDYSTSRCHPI
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                 Integrin alpha-M.
Extracellular (Potential)
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                                                                                   Cytoplasmic (Potential)
FG-GAP 1.
FG-GAP 2.
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/FTIG=VSP 010473.
N -> S (in Ref. 2).
V -> G (in Ref. 2).
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(GlcNAc...
(GlcNAc...
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                                                                                                                                                                                                                                                                                                                                                                                                                    By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
N-linked (GlCNAC.)
N-linked (GlCNAC.)
N-linked (GlCNAC.)
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FG-GAP
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                                                                                                                                                                                                                                        2,
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                                                                                                                                                                                       8F785695D4074CA5 CRC64;
                                pathway;
   GO, GO:0008305; C:integrin complex; IEA.
GO, GO:0007229; P:integrin adhesion; IEA.
GO, GO:0007229; P:integrin-mediated signaling pat
InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; VWF.A.
Pfam; PF001839; FG-GAP; 2.
Pfam; PF001839; FG-GAP; 2.
Pfam; PF001839; FG-GAP; 2.
Pfam; PF001839; WA; 1.
PRINTS; PR01185; INTEGRINA.
PRINTS; PR01185; INTEGRINA.
PRINTS; PR00191; Int. alpha; 5.
SWART; SM00191; Int. alpha; 5.
                                                                                                                                                                                                            Query Match 74.3%; Score 4371; DB 2; Best Local Similarity 72.6%; Pred. No. 3.5e-282; Matches 826; Conservative 150; Mismatches 159;
                                                                                                                                               PROSITE; PS00242; INTEGRIN ALPHA; 1. PROSITE; PS50234; VWFA; 1. Cell adhesion; Integrin; Transmembrane
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GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR
             QNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPL
                                                          PRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLF
                                                                                                           HGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTVGAQGHVLLLRSQ
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          090130;
01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0MR-2004 (TrEMBLrel. 26, Last annotation update)
Integrin beta 2 alpha subunit
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VPVRLNQTVIWDRPQVIFSENLSSTCHTKERLPSHSDFLABLRKAPVVNCSIAVCQRIQC 1017
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                CPLPRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAV
                                                                                                                                                                                                                            420 YLFHGISELGISPSHSQRIAGSQLSPRLQYRGQSLSGGQDLTWDGLMDLAVGAQGHVFLL
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                                                   QINNFEALKTIONOLREKIFALEGTOTGSSSSFEHEMSOEGFSAALTSNGPLLSTVGSYD
                                                                                                       WAGGVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVA
                                                                                                                                                         MFRQNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSV
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Catarrhini, Hominidae, Homo.
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P20702; Q81VA6;
01-FEB-1991 (Rel. 17, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Integrin alpha-X precursor (Leukocyte adhesion glycoprotein alpha chain) (Leukocyte adhesion receptor p150,95) (CD11c)
Name=ITGAX; Synonyms=CD11C;
Homo sapiens (Human).
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Primates;
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Mammalia; Eutheria;
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Led J.-K., Schook L.B., Rutherford M.S.;
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
L. SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
L. SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
EMBL; U40072; AAB16869.1; -
GO; GO:0008305; C:integrin complex; IEA.
GO; GO:0007160; P:cell-matrix adhesion; IEA.
InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; VWP_A.
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
NCBL TaxID=9823;
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Pfam; PF001839; FG-GAP; 3.
Pfam; PF01082; VWA; 1.
PRINTS; PR01185; INTEGRINA.
SMART; SM00191; Int alpha; 4.
SMART; SM00327; VWA; 1.
PROSITE; PS50234; VWFA; 1.
NON_TER
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Summe=CD11b,
Sus scrofa (Pig).
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**Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
**Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
**Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
**Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
**A pitschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
**A pitschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
**A pitschul S.F., Farmer A.A., Rubin G.M., Hong L.,
**Dratchenco M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
**Brownstein M.J., Usdin T.B., Tochhyuki S., Carninci P., Prange C.,
**Raha S.S., Loquellano N.A., Perers G.J., Abramson R.D., Mullahy S.J.,
**Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
**A pitschad S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
**A pitschad S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
**A hiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
**B Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
**B Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
** Roberzation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its wise by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
MEDLINE=88166645; PubMed=3327687; Corbi A.L., Miller L.J., O'Comnor K., Larson R.S., Springer T.A.; Corbi A.L., Miller and complete primary structure of the alpha subunit of a leukocyte adhesion glycoprotein, p150,95."; EMBO J. 6:4023-4028(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Integrin alpha-X/beta-2 is a receptor for fibrinogen. It recognizes the sequence G-P-R in fibrinogen. It mediates cell-cell interaction during inflammatory responses. It is especially important in monocyte adhesion and chemotaxis. Submit: Heterodimer of an alpha and a beta subunit. Alpha-X associates with beta-2.

SUBCELIGIAR LOCATION: Type I membrane protein.

TISSUE SPECIFICITY: Predominantly expressed in monocytes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    granulocytes.

DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins with I-domains do not undergo protease cleavage.

SIMILARITY: Belongs to the integrin alpha chain family.

SIMILARITY: Contains 7 FG-GAP repeats.

SIMILARITY: Contains 1 VWFA domain.
                                                                                                                                                                              MEDLINE=90153906; PubMed=2303426;
Corbi A.L., Garcia-Aguilar J., Springer T.A.;
"Genomic structure of an integrin alpha subunit, the leukocyte p150,95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 20-43.

MEDLINE=87167596; PubMed=3549901;
Miller L.J., Wiebe M., Springer T.A.;
"Purification and alpha subunit N-terminal sequences of human Mac-1 and pls0,95 leukocyte adhesion proteins.";
J. Immunol. 138:2381-2383(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                  Corbi A.L., Garcia-Aguilar J., Springer T.A., J. Biol. Chem. 265:12750-12751(1990).
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J. Biol. Chem. 265:2782-2788(1990).
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SEQUENCE FROM N.A.
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SEQUENCE FROM TISSUE=Blood;

ERRATUM.

EMBL; M81695; AAA59180.1; -.

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PROSITE; PS00242; INTEGRIN_ALPHA; 1.
PROSITE; PS50234; VWFA; 1.
3D-structure; Calcium, Cell adhesion; Direct protein sequencing; Glycoprotein; Integrin; Magnesium; Polymorphism; Receptor; Repeat; Signal; Transmebrane.
SIGNAL
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Extracellular (Potential).
Potential.
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(in Ref. 4).
(in Ref. 1).
(in Ref. 4).
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T -> A (in Ref. 4)
T -> S (in Ref. 4)
                                                                                                                                                                                                                              MIM; 151510; -. Octobroller; TAS. GO; GO:0008305; C:integrin complex; TAS. GO; GO:0004802; F:receptor activity; TAS. GO; GO:0007155; P:cell adhesion; TAS. GO; GO:0009887; P:organogenesis; TAS. InterPro; IPR000413; Integrin_alpha.
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M29482; AAAS1620.1; JOINED.
M29484; AAAS1620.1; JOINED.
M29484; AAAS1620.1; JOINED.
M29485; AAAS1620.1; JOINED.
M29486; AAAS1620.1; JOINED.
M29486; AAAS1620.1; JOINED.
M29486; AAAS18237.1; J
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Pfam, PF00357; Integrin_alpha; 1.
Pfam, PF00092; VWA, 1.
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PRINTS; PR00453; VWFADOMAIN.
SMART; SM00191; Int alpha; 5.
SMART; SM00327; VWA; 1.
                                                                                                                                                           PIR; A36584; RWHU1C.
PDB; 1N3Y; X-ray; A=141-338.
Genew; HGNC:6152; ITGAX.
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                 PVLRVKAIMEFNPREVARNVFECNDOVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVT
                                        YDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
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MEDLINE=20187620; PubMed=10722744;
Noti J.D., Johnson A.K., Dillon J.D.;
"Structural and functional characterization of tigene CD11d. Essential role of Spl and Sp3.";
J. Biol. Chem. 275:8959-8969(2000);
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16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0TJ-2004 (Rel. 44, Last annotation update)
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                                                                      MEDLINE=99059842; PubMed=9841932; Grayson M.H., Van der Vieren M., Sterbinsky S.A., Michael Gallatin W., Hoffman P.A., Staunton D.E., Bochner B.S.; "alphadbeta2 integrin is expressed on human eosinophils and functions as an alternative ligand for vascular cell adhesion molecule I (VCAM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Type I membrane protein.
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: Expressed moderately on myelomonocytic cell lines and subsets of peripheral blood leukocytes and strongly on tissue-specialized cells, including macrophages foam cells within atherosclerotic plaques, and on splenic red pulp macrophages. DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins with I-domains do not undergo protease cleavage.
SIMILARITY: Belongs to the integrin alpha chain family.
SIMILARITY: Contains 1 VWFA domain.
                                                                                                                                                                                                                                                                                                                                        EMBL; U37028; AAB38447.1; EMBL; U40274; AAB60634.1; EMBL; U40274; AAB60635.1; EMBL; U40275; AAB60635.1; EMBL; U40277; AAB60637.1; EMBL; U40277; AAB60637.1; EMBL; U40279; AAB60637.1; EMBL; U40279; AAB60638.1; EMBL; U40278; AAB60638.1; EMBL; U40278; AAB60638.1; GENEY; P11215; 1BHQ. EMBL; U40278; AAB60638.1; Genew, HONC: 64.6; ITGAD. MIM; 602453; C: integrin complex; TAS. GO; GO:0008305; C: integrin complex; TAS. GO; GO:00016337; P:cell-matrix adhesion; NAS. GO; GO:0007160; P:cell-matrix adhesion; NAS. InterPro; IPR00413; Integrin_alpha.
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Pfam; PF00357; Integrin_alpha; 1.
Pfam; PF00092; VWA; 1.
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PRINTS; PR00453; VWFADOMAIN.
SMART; SM00191; Int alpha; 5.
SMART; SM00327; VWA; 1.
Gene 171:291-294(1996).
                                                  INTERACTION WITH VCAM1
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InterPro; IPR002035; VWF_A.
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NR Res. 11:167-180(2004).

-: SUNCELLUIAR LOCATION: Type I membrane protein (By similarity).

-: SIMILARITY: Belongs to the integrin alpha chain family.

EMBL: AKI31133: BAD21333:1;

GO: GO:0009897; C:excernal side of plasma membrane; IDA.

InterPro; IPR000413; Integrin_alpha.
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                                                             PVLRVKAIMBENPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVT
                                                                                                   661 YDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNF
                                                                                                                                      SLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVG
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            PRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLF
                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Last sequence update)
Last annotation update)
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GGKAS4;

GS-JUL-2004 (TrEMBLrel. 27, Las

GS-JUL-2004 (TrEMBLrel. 27, Las

GS-JUL-14 procein (Fragment).

Name=mFLJ00114;

Mus musculus (Mouse)
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                                                                                              PROSITE; PS00242; INTEGRIN ALPHA; UNKNOWN_1.
PROSITE; PS50234; VWFA; 1.
Cell adhesion; Integrin; Transmembrane.
NON TER 138 AA; 131248 NW; B8D93107BDB84178 CRC64;
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pfam; PF01839; FG-GAP; 3.
pfam; PF00357; Integrin_alpha; 1.
pfam; PF00092; WWA; 1.
PRINTS; PR01185; INTEGRINA.
SMART; SM00191; Int_alpha; 5.
SWART; SM00191; Int_alpha; 5.
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YDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNF 720
GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR
                                                                                                          QNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLLGAPHYYEQTRGGQVSVCPL
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Sciurognathi, Muridae, Murinae, Mus
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05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
105-JUL-2004 (Rel. 45) Last annotation update)
105-JUL-2004 (Rel. 46) Last annotation update)
105-JUL-2004 (Rel. 47, Last annotation update)
105-JUL-2004 (Rel. 47, Last annotation update)
105-JUL-2004 (Rel. 47, Last adhesion glycoprotein lalpha chain) (Leukocyte adhesion receptor pl50,95) (CD11c).
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Mammalia, Eutheria, Rodentia,
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TISSUE=Dendritic cell;
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Mus musculus (Mouse)
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LACESASSTEVSGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSE
                            NNMPRTNKTEFQLELEVKYAVYMVTSHGVSTKYLNFTASE-NTSRVMQHQYQVSNLGQR
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                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S., Saga Y., Kitamura H., Nakagawa T., Nagase T., Ohara O., Koga H.;

Prediction of the Coding Sequences of Mouse Homologues of FLJ Gene:
The Complete Nucleotide Sequences of 110 Mouse FLJ-homologous cDNAs Identified by Screening of Terminal sequences of cDNA Clones Randomly Sampled from Size-Fractionated Libraries.";
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.

EMBL, AKI31133; BAD21383.1;

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01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
MFLJ00114 protein (Fragment).
MFLJ00114.
MRLJ00115.
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae, Musines, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese, Musinese,
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1169 AA; 129150 MW; C616412033C219A6 CRC64;
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                 This SWISS-PROT entry is copyright, It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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RVHFTFNNFISTSSPLSLGSVRQLRGYTYTASAIKHVITELFTTQSGARQDATKVLIVI
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                                                                                                                                                Gaps
                                        19;
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Score 3310.5; DB 1;
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----heg 303;
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LRSPLBAVNMSLGLSLVTATNNAQLLACGPTAQRACVKNMYAKGSCLLLGSSL-QFIQAV 139
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al Similarity 57.5%; Pred. No. 1.6e-206;
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RA Gallatin W.W., VanderVieren M., Kilganmon P.D., Dietsch G.,

RA Gallatin W.M.,

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"CAMILATINE blood (By similarity).

"CAMILATINE LOCATION: Type I membrane protein (By similarity).

"CAMILARITY: Contains do not undergo protease cleavage.

"I SUBLITY: Contains 1 VWFA domain.

"CAMILARITY: Contains 1 VWFA domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMEL; AF021334; AAF21241.1; -

R HSSP; P11215; 1BHQ.

In therPro; 1PR000043; VWF A.

R Ffam; PF01399; FG-GAP; 3.

R Pfam; PF01095; VWA; 1.

R PRINTS; PR01185; Integrin_alpha; 1.

R PRINTS; PR01185; Integrin_alpha; 1.

R PRINTS; PR00453; VWFADOMAIN.

R SMART; SM00191; Int_alpha; 5.

SMART; SM00191; Int_alpha; 5.

RWART; SM00191; Int_alpha; 6.

RWART; SM00191; Int_alpha; 6.

RWART; SM00191; Int_alpha; 6.

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IAVCORIOCDIPFFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLP
                                                                                 GQGAFVRSQTETKVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMMSE
                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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Extracellular (Potential)
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Cytoplasmic (Potential)
FG-GAP 1.
                                                                                                                                                                                                                                                                    05-JUL-2004 (Rel. 44, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Potential.
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                                                                                                                                                                                                                                                                                                                                         Integrin alpha-D precursor
Name=Itgad;
                                                                                                                                                                                                                                     STANDARD;
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REPEAT
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SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins with I-domains do not undergo protease cleavage.
SIMILARITY: Belongs to the integrin alpha chain family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene 325:97-101(2004).
-!- FUNCTION: Integrin alpha-L/Deta-2 is a receptor for ICAM1, ICAM2,
-!- FUNCTION: Integrin alpha-L/Deta-2 is a variety of immune phenomena
ICAM3 and ICAM4.
Including leukocyte-endothelial cell interaction, cytotoxic T-cell
including leukocyte-endothelial cell interaction, cytotoxic T-cell
mediated killing, and antibody dependent killing by granulocytes
and monocytes (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Integrin alpha-L precureor (Leukocyte adhesion glycoprotein LFA-1
alpha chain) (LFA-IA) (Leukocyte function associated molecule 1, alpha chain) (CD11a).
                                                                                                                                                                                                                                                                                                                                                                                                             PPFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLPGQGAFVRSQTE
                                                                                                                                                                           782 PREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEVS
                                                                                                                                                                                                                                  GALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRTNKTEFQ
                                                                                                                                                                                                                                                    LELPVKYAVYMVVTSHGVSTKYLNFTASENTSR-VMQHQYQVSNLGQRSLPISLVFLVPV
                                                                                                                                                                                                                                                                                                              RINQTVIMDREQVIFSENLSS-TCHTKERLPSHSDFLABLRKAPVVNCSIAVCQRIQCDI
                                                                                                                 LVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVGG
                                                                                                                                   VLRVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVTY
                  DLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus (Bovine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECUENCE FROM N.A.

PubMed=14697514; DOI=10.1016/j.gene.2003.09.043;

Pett T. ZecAhinon L., Baise E., Desmecht D.;

Fett Glos taurus) Colla-encoding coNA: molecular cloning, characterisation and comparison with the human and murine
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NCBI_TaxID=9913;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 PIRLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLRQQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 OKEPBALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEWVSTVMEQLKKSKTLFSLMQYSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 FNLDTENAMTFQENARG--FGQSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSTGSCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 YNLDVRHVQNFSFPLAGRHFGYRVLQV-GNGVVVGAPSE---GNSMGNLYQCQPETGDCL
                                                                                                                           PROSITE; PSO0242; INTEGRINALPHA; 1.
PROSITE; PSO0242; INTEGRINALPHA; 1.
Calcium; Cell adhesion; Glycoprotein; Integrin; Magnesium; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Potential)
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                                                                                                                                                                                 Integrin alpha-L.
Extracellular (Potential)
Potential.
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FG-GAP 1.
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1.7e-95;
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FG-GAP 4.
FG-GAP 5.
FG-GAP 7.
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SIMILARITY: Contains 7 FG-GAP repeats. SIMILARITY: Contains 1 VWFA domain.
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                                                                                                                                                                              Potential.
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FG-GAP 2.
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34.6%;
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SIGNAL
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function associated molecule 1, alpha

chain) (LFA-1A) (Leukocyte

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429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ERLPSHSDFLAEIRKAPVVNCSIAVCQRIQCDIPFFGIQEEFNATLKGNLSFDWYIKTSH 1046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----SCSFGT--EFRCPIDF---RQEILVQVNGMVELRGTIKAS- 1042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1047 NHLLIVSTAEILFNDSVFTLLPGQGAFVRSQTETKVEPPEVPNPLPLIVGSSVGGLLLLA 1106
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 LLTDGEKFGDPLGYEDVIPELD-REGVIRYVIGVGDAFRSEKSRQELNTVASKPPRDHVF
                                               QINNFEALKTIQNQLREKIFAIEGTQTGSSSSFEHEMSQEGFSAAITSNGPLLSTVGSYD
                                                                                                                    WAGGFLDLKADLKSSTFVGNEPLTVESRAGYLGYTVTWLPSRGTMSLLATGAPRYQHVGR
                                                                                              WAGGVF-LYTSKEKSTFINMTRVDSDMNDAYLGYAAA-IILRNRVQSLVLGARRYQHIGL
                                                                                                                                             VAMFRO--NTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGG
                                                                                                                                                                  VLLFQQPKRGGPWSQIQBIDGIQIGSYFGGELCGVDVDRDGETELLLIAAPLYYGEQRGG
                                                                                                                                                                                           QVSVCPLPRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDN
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TTAL HUMAN STANDARD; PRT; 1170 AA.
P20701; 043746;
01-PEB-1991 (Rel. 17, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Integrin alpha-L precursor (Leukocyte adhesion glycoprotein LFA-1

17AL HUMAN 1D 17AL HUMAN 1D 17AL HUMAN 1D 01-FEB 1D 01-NOV-1D 01-OCT-1D 11Legri

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                               SEQUENCE FROM N.A. (ISOPORM 1), AND PARTIAL SEQUENCE.
MEDLINE=89139587; PubMed=2537322;
Larson R.S., Corbi A.L., Berman L., Springer T.;
"Primary structure of the leukocyte function-associated molecule-1
alpha subunit: an integrin with an embedded domain defining a protein
superfamily.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qu A., Leahy D.J.; The role of the divalent cation in the structure of the I domain from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDITA I-domain.";
J. Mol. Biol. 292:1-9(1999).
-!- FUNCTION: Integrin alpha-L/beta-2 is a receptor for ICAMI, ICAM2, ICAM3 and ICAM4. It is involved in a variety of immune phenomena including leukocyte-endothelial cell interaction, cytotoxic T-cell mediated killing, and antibody dependent killing by granulocytes
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'Intsug Specificity: Leukocytes.

'DOMAIN: The integrin 1-domain (integrin service) with I-domains do not undergo protease cleavage.

'SIMILARITY: Belongs to the integrin alpha chain family.

SIMILARITY: Contains 7 RG-GAP repeats.

SIMILARITY: Contains 1 WFA domain.

'I SIMILARITY: Contains 1 WFA domain.

'DATABASE: NAME=PROW; NOTE=CD guide CD11a entry;

WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd11a.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                           from
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MEDLINE=99425288; PubMed=10493852;
Kallen J., Welzenbach K., Ramage P., Geyl D., Kriwacki R., Legge G.,
Cottens S., Weizz-Schmidt G., Hommel U.,
"Structural basis for LFA-1 inhibition upon lovastatin binding to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qu A., Leahy D.J., "Crystal structure of the I-domain from the CD11a/CD18 (LFA-1, alpha beta 2) integrin."; Proc. Natl. Acad. Sci. U.S.A. 92:10277-10281(1995).
                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOPORM 2).

BEDLINE=99425270; PubMed=10493829;
Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon R., Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L., Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S., Eichler E.B., Harris P.C., Venter J.C., Adams M.D.; "Genome duplications and other features in 12 Mb of DNA sequence human chromosome 16p and 16q"";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 153-335, AND REVISION MEDLINE=96036067; PubMed=7479767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 associates with beta-2.
SUBCELLULAR LOCATION: Type I membrane protein.
ALTERNATIVE PRODUCTS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId=P20701-2; Sequence=VSP_002738;
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                                                                                                                                                                                                                                                              Cell Biol. 108:703-712(1989).
                                  Name=ITGAL; Synonyms=CD11A;
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the CD11a/CD18 integrin.";
Structure 4:931-942(1996),
                                                                                                            NCBI_TaxID=9606;
                       (CD11a).
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RGGOVSVCPLPRGQRARWQCDAV--LYGEQGOPWGRFGAALTVLGDVNGDKLTDVALGAP 528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141 LQGRPGFQECIKG----NVDLVFLFDGSMSLQPDEFQXILDFMXDVMKKLSNTSYQFAAV 196
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Query Match 26.3%; Score 1547.5; DB 1; Length 1170;
Best Local Similarity 34.3%; Pred. No. 7.2e-94;
Matches 403; Conservative 210; Mismatches 460; Indels 101; Gaps
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                     the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PIR; S03308; S03308.
PIR; S03308; S03308.
PIB; ICQP, X-ray; A/B=153.334.
PDB; IDGQ; NWR; A=149.336.
PDB; ILKA; X-ray; A-B=153.331.
PDB; IMCN; X-ray; A-B=153.331.
PDB; IMCN; X-ray; A-B=153.331.
PDB; IMQ9; X-ray; A-B=152.330.
PDB; IZCO; X-ray; A-B=150.336.
PDB; IZCO; X-ray; A-B=150.336.
PDB; IZCO; X-ray; A/B=150.336.
PDB; IZCO; X-ray; A/B=1
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                                                                                                                                                                      RGGRVFIY----QRRQLGFEEVSELQGDPGYPLGRFGEAITALTDINGDGLVDVAVGAP
                                            GEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDUTWDGLVDLTV
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Lybphocyte function-associated antigen 1 alpha subunit CD11a.
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disease Town T., Thumbiket P., Kannan M.S., Maheswaran S.K.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
-- SUBCELDULAR LOCATION: Type I membrane protein (By similarity).
--- SIMELARITY: Belongs to the integrin alpha chain family.
--- InterPro; IPR000413; Integrin_alpha.
InterPro; IPR000413; Integrin_alpha.
Ffam; PF001839; FG-GAp; I.
Pfam; PF00092; VWA, I.
Pfam; PF00092; VWA; I.
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NCBI_TaxID=9913;
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                                                                                                                                                                     106;
                                                                                                                             Query Match
26.3%; Score 1546; DB 2; Length 11
Best Local Similarity 34.3%; Pred. No. 9.1e-94;
Matches 405; Conservative 202; Mismatches 469; Indels
                                                                                                   7B8D8AFBA896C9DF CRC64;
PRINTS; PRO0453; VWFADOMAIN.
SMART; SM00191; Int. alpha; 5.
SMART; SM00327; VWA; 1.
PROSITE; PS00242; INTEGRIN ALPHA; 1.
PROSITE; PS50234; VWFP; 1.
Cell adhesion; Integrin; Transmembrane.
SEQUENCE 1166 AA; 128723 WW; 7B8DBA
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                                                                        LLLRSQPVLRVKAIMERNPRBVARNVFBCNDQVVKGKEAG-EVRVCLHVQK--STRDRLR
                                                                                                                                                                                       EGOIQSVVIYDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPV
                                                                                                                                                                                                                                              SPIVLRINFSL - - - VGTPLS - - AFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLS
                                                       VSVCPLPRGQRARWQCDAVLYGEQGPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNR
                                                                                                            GAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTVGAQGHV
                                                                                                                              417 AMFRO -- NTGMWESNANVKGTOLGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGO
                (Rel. 21, Created)
(Rel. 21, Last sequence update)
(Rel. 44, Last annotation update)
Main-1, precursor (Leukocyte adhesion glycoprotein LFA-1)
(LFA-1A) (Leukocyte function associated molecule 1, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=91266576; PubMed=2051027;
Kaufmann Y., Tseng E., Springer T.A.;
"Cloning of the murine lymphocyte function-associated molecule-1
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SEQUENCE FROM N.A.
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chain) (CD11a)
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                                                                                                           RLPSHSDFLAELRKAPVVNCSIAVCQRIQCDIPFFGIQEEFNATLKGNLSFDWYIKTSHN
                                                                                                                                                                 HILIVSTAEILFNDSVFTLLPGQGAFVRSQTETKVEPFEVPNPLPLIVGSSVGGLLLLAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
           SCNNEDSSLLEDNSATTS-----IPVMYPINVLTKDQENSTLYISFTFKSPRIHHVKH
                                                   QYQV----SNLGQRSLPISLVFLVPVRLNQTVI----WD----RPQVTFS-ENLSSTCHTKE
                                                                         AAQ90015;

0.2-MAR-2004 (TrEMBLrel. 27, Created)

0.2-MAR-2004 (TrEMBLrel. 27, Last sequence update)

0.2-MAR-2004 (TrEMBLrel. 27, Last annotation update)

1.ymphocyte function-associated antigen 1 alpha subunit CD11a.

Bos taurus (Bovine)

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26.3%; Score 1546; DB 2; Length 1166; 34.3%; Pred. No. 9.1e-94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Dileepan T., Thumbikat P., Kannan M.S., Maheswaran S.K.;
Molecular cloning and sequencing of bovine CD11a.";
submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AY382558; AAQ90015.1; -.
SEQUENCE 1166 AA; 128723 MW; 7BBDBAFBA8996C9DF CRC64;
                                                                                                                                                                                                                                            ---SEGGPPGAEPO 1137
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Best Local S:
Matches 405;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 297 FQINNFBALKTIQNQLREKIFALEGTQTGSSSSFEHEMSQEGFSAAITSNGPLLSTVGSY 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :: || || : |: || || 310 KILDTPEKLKDLFTDLQRRIYAIEGTNRQDLTSFNMELSSSGISADLSKGHAVVGAVGAV 369
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|GRVFTY---QRRQSLFEMVSELQGDPGYPLGRFGAAITALTDINGDRLTDVAVGAPLEE-
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662 QGRLLANLSYTLQLDGHRMRSRGLFPDGSHELSGNTSITP-DKSCLDFHFHFPICLQDLI
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                                                                                                                                                                                        (Potential)
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                                                                                                                                                                                                                                                                                                     26.0%; Score 1527.5; DB 1; Length 1163; 34.1%; Pred. No. 1.5e-92;
                                                                                                                                                                                                                                                                                                                                       89;
                                                                                                                                    (Potential)
                                                                                                                                                   (Potential)
                                                                                                                                                                                                                                                                                                                                217; Mismatches 463; Indels
                                                                                                                                                                                                                                                          156 N-linked (GlcNAc. .) (Pote 128343 MW; A7A3078489E8232F CRC64;
                By similarity.
By similarity.
By similarity.
N-linked (GlCNAC.)
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                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                   MEDLINE=85188276; PubMed=3887182; SEQUENCE OF 24-42.

MEDLINE=85188276; PubMed=3887182; Springer T.A., Teplow D.B., Dreyer W.J.; Sequence homology of the LFA-1 and Mac-1 leukocyte adhesion glycoproteins and unexpected relation to leukocyte interferon."; Integrin alpha-L/beta-2 is a receptor for ICAM1, ICAM2, including leukocyte-endothelial cell interaction, cytotoxic T-cell mediated killing, and antibody dependent killing by granulocytes and monocytes. Mice expressing a null mutation of the alpha-L subunit gene demonstrate impaired tumor rejection and impaired
                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Type I membrane protein.

SUBCELLULAR LOCATION: Type I membrane protein.

TISSUE SPECIFICITY: Leukocytes.

DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins with I-domains do not undergo protease cleavage.

SIMILARITY: Belongs to the integrin alpha chain family.

SIMILARITY: Contains 7 FG-GAP repeats.

SIMILARITY: Contains 1 VWFA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Integrin alpha-L.
Extracellular (Potential)
Potential.
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alpha-subunit and its expression in COS cells."; J. Immunol. 147:369-374(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similarity.
similarity.
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FG-GAP 4.
FG-GAP 5.
FG-GAP 7.
FG-GAP 7.
Potential.
Potential.
GPFKR motif.
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HSSP; P20701; IDGO.
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                                                                                                 940 YOVSNLGORSLPISLVFLVPVRLNOTVIMDRPQ----VTFSENLSS----TCHTKE-RLP 990
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                                          768 TESEMSLDCLVVGGP-----REFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQN 821
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| SUMMARIES | ID             | AAW65090   | AAB07360 | AAU80252 | ABG61469 | AA014428 | ADD25615 | AAR04136 | ADM99589 | ADP12435 | ADP44061 | ADN02004 | ADQ17510 | AAR07120 | AAW65091 | AAB07361 | ABG61470 | ABU07406 | ADG32005 | AAR78166 | AAW23049 | AAW57491 | AAW65089 | AAW72825  | AAW73342 | AAR07359 | Cocyona            |
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ALIGNMENTS

psoriasis;

11b subunit; 93US-00173497. 94US-00286889. 94US-00362652. 95US-00485618. rheumatoid arthritis. Homo sapiens. 07-JUN-1995; 05-AUG-1994; 21-DEC-1994; 23-DEC-1993; US5728533-A. 17-MAR-1998 RESERVED TO THE SECOND OF THE

Gallatin WM; (ICOS-) ICOS CORP. Van Der Vieren M,

WPI; 1998-206565/18.

Screening assay for modulators of integrin binding - using immobilised or labelled alpha-d polypeptide, useful for, e.g. treating type-I diabetes.

Example 5; Fig 1A-D; 106pp; English.

This sequence represents a human beta-integrin CD11b subunit which is used to describe a method for identifying compounds that modulate the interaction of the beta-integrin alpha-d subunit with a binding partner of alpha-d which involves contacting an alpha-d polypeptide with an alpha-d binding partner, one of which is immobilised and the other of which is labelled, in the presence of a test compound, and determining if the compound affects binding between the alpha-d polypeptide and alpha-d binding partner, where the alpha-d polypeptide is alpha-d or its fragment comprising the cytoplasmic, transmembrane or extracellular domain of alpha-d. Compounds that modulate alpha-d binding could be used to treat

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Integrins are a class of membrane-associated molecules that participate in cellular adhesion. Integrins are made up of an alpha subunit and a beta subunit. One class of human integrins are restricted to expression in white blood cells and have a common beta2 subunit: the leukocyte integrins. Leu-CAMS, leukointegrins or beta2 integrins. Beta2 integrins have an important role in immune and inflammatory responses. The present protein sequence is the human integrin alpha subunit CD11D. This sequence was used in an alignment to identify a novel beta2 integrin alpha subunit; alpha d (AAA6014 and AAB07159). The present sequence has approximately 60% identity to the protein sequence of alpha d. The Alpha d gene and protein may be useful in therapy for diseases linked to aberrant alpha d function e.g. Type I diabetes, atherosoclerosis, multiple sclerosis, strima, psoriasis, lung inflammation, acute respiratory distress syndrome, rheumatoid arthritis and leukocyte adhesion deficiency clinibition of macrophage infiltration at the site of a central nervous system injury. The monoclonal antibodies can also be used to detect and diagnose Crohn's disease
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This invention relates to a modified integrin-I or integrin I-like domain polypeptide comprising at least one disulfide bond so that the domain is stabilised in a desired conformation. The polypeptide of the invention may have antiinflammatory or imunosuppressive activities. The useful as immunogens to produce antibodies that selectively bind to integrin I-domain; and for identifying a modulator of integrin activity, or of inteartion of an integrin and a cognate ligand. The polypeptide of the invention, or antibodies (preferably anti-LFA-I antibody) is useful for treating or preventing an integrin mediated disorder which is an inflammatory or autoimmune disorder in a subject and for inhibiting the binding of an integrin to a cognate ligand such as Crohn's disease, binding of an integrin to a cognate ligand such as Crohn's disease, composition comprising the peptide of the invention is useful for composition comprising the peptide of the invention is useful for the infing an integrin disorder in a subject. The polypeptides and comprising the peptide of the invention is useful for and comprising the peptide of the invention is useful for and comprising the peptide of the invention is useful for and comprising the peptide of the invention is useful for and compress the integrin mediated disorder in a subject. The polypeptides and compress the composition comprises the composition of the polypeptides and compress the composition compress the composition compress the composition compress the composition compress the composition compress the composition compress the composition compress the composition compress the composition compress the composition compress the composition compress the composition compress the composition compress the composition compress the composition compress the composition compress the composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition compo
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The invention relates to promoting locomotor recovery, inhibiting concomotor damage, limiting locomotor impairment, or limiting autonomic and sensory dysfunction following spinal cord injury by administering an anti-alpha d (Beta2 integrin alpha2 subunit) monoclonal antibody to a spinal cord injury victim. The method also involves the use of a ligand selected from ICAM-R or VCAM-1 (intracellular cell adhesion molecule, vascular cell adhesion molecule). The method is useful for promoting locomotor recovery, inhibiting locomotor damage, limiting locomotor impairment, or limiting autonomic and sensory dysfunction following spinal cord injury. The appinal cord injury comprises compression of the spinal cord. The antibodies are also useful for reducing inflammation at the site of a central nervous system injury. The specification also details the identification of Beta2 integrins constitution and indiseases such as IAAD (leukocyte adhesion deficiency, and indicates such as IAAD (leukocyte adhesion deficiency, and integrins and indicates and integrins and indicates and integrins and indicates and integrins and indicates and integrins and indicates and integrins and indicates and integrins and indicates and integrins and indicates and integrins and integrins and integrins and integrins and integrins and integrins and integrins and integrins and integrins and integrins and integrins and integrins and integrins and integrins and integrins and integrins and integrins and integrins and integrins and integrins and integrins and integrins and integrins and integrins and integrins and integrins and integrins and integrins and integrins and integrins and integrins and integrins and integrins and integrins and integrins and integrins and integrins and integrins and integrins and integrins and integrins and integrins and integrins and integrins and integrins and integrins and integrins and integrins and integrins and integrins and integrins and integrins and integrins and integrins and integring and integring and integring and 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Use of an anti-alpha-d monoclonal antibodies for promoting locomotor recovery, inhibiting locomotor damage, limiting locomotor impairment, or limiting autonomic and sensory dysfunction following spinal cord injury.
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                                                                                    Gaps
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                                                  Length 1153;
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                                                                                    7; Mismatches
                                                  Score 5852;
Pred. No. 0;
                                                  99.5%;
99.2%;
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                                                                   Similarity
                Sequence 1153 AA;
                                                                     Best Local Sim
Matches 1128;
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Van Der Vieren

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                                                                                                                                                                                                  KVEPFEVPNPLPLIVGSSVGGLLLIALITAALYKLGFFKRQYKDMMSEGGPPGAEPQ 1137
                                                                                                                                                                                                                                        FFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLFGQGGAFVRSQTET
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(first entry)
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Matches 1128; Conservative
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CENT BLOOD
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                 Score 5852;
Pred. No. 0;
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The invention comprises structurally biased variant integrin inserted (1)

domain proteins, wherein the alterations to the protein occur in at least

two nonontinuous regions. Specifically the the variant integrin I domain

proteins are structurally biased to exist in the open conformation. It

thereby altering the binding ability of the protein. The invention also

comprises nucleic acids encoding the variant integrin I domain proteins.

The integrin I domain proteins and nucleic acids are useful for treating,

preventing or suppressing integrin related inflammatory and immunological

comprises for the proteins and nucleic acids are useful for treating,

fisorders (e.g. rheumantoid arthritis). The variant integrin I domain

proteins and nucleic acids can also be used for treating; ischaemia/

reperfusion (e.g. hypovolemic shock); infarction, cerebral shock, viral

infaction; and cancer. The variant integrin I domain nucleic acids and

proteins may be used in gene therapy, as vaccines and to screen for

bloactive agents. The present amino acid sequence represents the Mac-1

alpha subunit of integrin
Mac-1; integrin alpha subunit; variant integrin inserted domain protein; open conformation; integrin related inflammatory disorder; integrin related inmunological disorder; rheumatoid arthritis; ischaemia; reperfusion; hypovolemic shock; infarction; cerebral shock; viral infection; cancer; gene therapy; vaccine;
                                                                                                     KVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMMSEGGPPGAEPQ 1137
                                                                                                                                                Gaps
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                                                            RLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLRQQPQK
                                                                                                           FPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEBF
                                                                                                                                            RIHFTFKEFONNPNPRSLIKPITOLLGRTHTATGLRKVVRELFNITNGARKNAFKILFLL
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                                                                                             FPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEWVSTVMEQLKKSKTLFSLMQYSEEF
             FNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSTGSCEPI
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mutated human igG1 immunoglobulin hinge region polypeptide, derived from mutated human igG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues, where the mutated human igG1 immunoglobulin hinge region polypeptide contains no more than one cysteine residue; and a mutated human igG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues; where the mutated human igG1 immunoglobulin hinge region polypeptide contains no cysteine residues immunoglobulin hinge region polypeptide contains capable of at least one immunoglobulin hinge region polypeptide contains dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a binding domain-immunoglobulin fusion protein comprising a binding domain polypeptide that is fused to an immunoglobulin havy chain cHz constant region polypeptide, an immunoglobulin heavy chain cHz constant region polypeptide that is fused to the hinge region polypeptide that is fused to the CHZ constant region polypeptide that is fused to the CHZ constant region polypeptide comprises: a wild-type human IgG1 immunoglobulin hinge region polypeptide, a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues; where the mutated human IgG1 immunoglobulin hinge region polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fixation;
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Binding domain, immunoglobulin, fusion protein, cytostatic; antiarthritic; immunosuppressive; antidiabetic; antithyroid; neuroprotective; hinge region; immunoglobulin heavy chain; CET2 constant region; 1991, antibody dependent cell-mediated cytocoxicity; ADCC; complement fixa malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma; rheumatoid arthritis; myaschenia gravis; Grave's disease; type I diabetes mellitus; multiple sclerosis; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Binding domain-immunoglobulin fusion protein-associated protein
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17-JAN-2002; 2002US-00053530.
03-JUN-2002; 2002US-0385691P.
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ð pharmaceutical composition comprising the binding domain-immunoglobulin fusion protein or polymucleotide and a carrier, and treating a subject having or suspected of having a malignant condition or a B-cell disorder. The binding domain-immunoglobulin fusion protein is useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, carcinoma or sarcoma, theumatoid arthritis, mysthenia gravis, Grave's disease, type I diabetes mellitus, multiple sclerosis or autoimmune disease. The present sequence is a binding domain-immunoglobulin fusion protein-associated protein sequence. Note: The sequence data for this patent formed part of the printed specification and is also available in electronic format directly from USPTO at sequence. In the printed specification by their SED ID number therefore none of the sequences can be explicitly identified. \$

Sequence 1153 AA,

o, 120 136 180 196 240 256 300 316 360 420 436 480 540 376 496 009 96 556 099 676 720 SLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVG 780 FNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSTGSCEPI RLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLRQQPQK RIHFTFKEFONNPNPRSLIKPITOLLGRTHTATGLRKVVRELFNITNGARKNAFKILFLL TDGEKFGDPLGYEDVIPELDREGVIRYVIGVGDAFRSEKSRQELNTVASKPPRDHVFQIN NFRALKTIQNQLREKIFAIEGTQTGSSSSFEHEMSQEGFSAAITSNGPLLSTVGSYDWAG 317 NFBALKTIQNQLREKIFAIEGTQTGSSSSFEHEMSQEGFSAAITSNGPLLSTVGSYDWAG GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR 377 GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR PVLRVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVT FNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSTGSCEPI FPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEWVSTVMEQLKKSKTLFSLMQYSEEF PRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLF HGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTVGAQGHVLLLRSQ PVLRVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVT YDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNF Gaps QNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPL QNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPL YDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSP1VLRLNF ·, Length 1153; Indels 7; 2; DB Score 5852; DB; Pred. No. 0; 7; Mismatches 99.5%; Query Match Best Local Similarity 99.2 Matches 1128; Conservative 17 61 17 121 181 197 241 257 301 481 557 361 421 437 497 541 601 661 721  $\delta$ d à Dp g Op à Db ŏ  $\delta$ ò Dp à D à q ò 셤 ò Db ò qq

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                                             GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR
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         GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR
                                QNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPL
                                                                                                       QNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPL
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                                                                                                                                                                             HGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTVGAQGHVLLLRSQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transplant rejection; immune system; rheumatoid arthritis; lupus; inflammatory bowel disease; multiple sclerosis; HIV; AIDS.
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                                                                                                                                                                                                                                                                                                                                                                                  Novel modified integrin protein having extracellular domains of integrin alpha and beta subunits or integrin alphaII and beta3 subunit, useful for treating integrin mediated disorders.
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Pred. No. 0;
7; Mismatches
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                                    /note= "Encoded by CCC"
 Location/Qualifiers
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11-SEP-2002; 2002US-0410135P.
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                                                                                                                                                                                          The present invention relates to diagnosing or monitoring transplant rejection, e.g. cardiac or kidney transplant rejection, in an individual comprises detecting the expression level of one or more genes. The methods, system and kits are useful in diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, srentransplant rejection or mechanical organ replacement rejection, in an individual. The method is also useful in assessing the immune status of an individual. The method are also useful in diagnosing and monitoring an individual involve the immune system, e.g. rheumatoid arthritis, lupus, inflammatory bowel diseases, multiple sclerosis, HIVAIDS or viral, bacterial or fungal infection. The present sequence represents a protein that is encoded by the mRNA of the invention.
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                                                                                                                  Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liv pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in an individual, comprises detecting the expression level
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  257 TDGEKFGDPLGYEDVIPBADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVN
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Pred. No. 0;
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                                         (EXPR-) EXPRESSION DIAGNOSTICS
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99.0%;
         2002US-00131831
2002US-00325899
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Best Local Similarity 99.0
Matches 1126; Conservative
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                                                                                                 WPI; 2004-400724/37.
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                                                               Wohlgemuth J,
         24-APR-2002;
20-DEC-2002;
                                                                           Rosenberg S;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RINQTVIWDRPQVIFSENLSSICHIKERLPSHSDFLABLRKAPVVNCSIAVCQRIQCDIP
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                                                                                                                                                                                                                                                                                                                                                                                                                 796 GPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QLELPVKYAVYMVVTSHGVSTKYLNFTASENTSRVMQHQYQVSNLGQRSPPISLVPI/VPV
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HGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTVGAQGHVLLLRSQ
                                                                                                                                                                                   YDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNF
                                                                                                                                                                                                                               YDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNF
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                                                                                         PVLRVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVT
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β

The present invention describes a method (MI) for identifying an inhibitor of HIV entry into a human host cell. (MI) comprises identifying an inhibitor of a cell surface polypeptide selected from CXCR-4 (352 an inhibitor of a cell surface polypeptide selected from CXCR-4 (352 amino acids, SEQ ID NO:10, ADP44059), CCR7 (378 amino acids, SEQ ID NO:12, ADP44059), CDIC (1163 amino acids, SEQ ID NO:12, ADP44069), CDIC (1163 amino acids, SEQ ID NO:12, ADP44069), CDIC (1163 amino acids, SEQ ID NO:24, ADP44069), CSF3R (836 amino acids, SEQ ID NO:24, ADP44065), CDE9 (199 amino acids, SEQ ID NO:26, ADP44067), CDV3 (199 amino acids, SEQ ID NO:26, ADP44067), CDV3 (199 amino acids, SEQ ID NO:26, ADP44073), CRPX (150 amino acids, SEQ ID NO:28, ADP44075), CCC (103 amino acids, SEQ ID NO:28, ADP44075), PZXI (150 amino acids, SEQ ID NO:28, ADP44077), RARA (150 amino acids, SEQ ID NO:30, ADP44087), CRPX (150 amino acids, SEQ ID NO:30, ADP44087), CRPX (150 amino acids, SEQ ID NO:30, ADP44087), CRPX (150 amino acids, SEQ ID NO:30, ADP44087), CRPX (150 amino acids, SEQ ID NO:30, ADP44087), CRPX (150 amino acids, SEQ ID NO:30, ADP44087), CRPX (150 amino acids, SEQ ID NO:30, ADP44087), CRPX (150 amino acids, SEQ ID NO:30, ADP44087), CRPX (150 amino acids, SEQ ID NO:30, ADP44087), CRPX (150 amino acids, SEQ ID NO:30, ADP44087), CRPX (150 amino acids, SEQ ID NO:30, ADP44087), ADP44083), ADP44081), or PTYZB (1009 amino acids, SEQ ID NO:30, ADP44083), ADP44081), or PTYZB (1009 amino acids, SEQ ID NO:30, ADP44083), ADP44083), ADP44081, or PTYZB (1009 amino acids, SEQ ID NO:30, ADP44083), ADP44081, or PTYZB (1009 amino acids, SEQ ID NO:30, ADP44083), ADP44083), ADP44081, or PTYZB (1009 amino acids, SEQ ID NO:30, ADP44083), ADP44083), ADP44083, A a human host cell useful for preventing and/or treating HIV infection, identifying an inhibitor of a cell surface polypeptide such as CXCR-4. SEQ ID NO 14; 133pp; English. 

Sequence 1163 AA;

RLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLRQQPQK 120 180 197 TDGEKFGDPLGYEDVIPELDREGVIRYVIGVGDAFRSEKSRQELNTVASKPPRDHVFQIN 300 257 317 360 377 420 437 480 497 540 FNLDTEELTAFRVDSAGFGDSVVQYANSWVVVGAPQKITAANQTGGLYQCGYSTGACEPI 79 301 NFEALKTIQNQLREKIFALEGTQTGSSSSFEHEMSQEGFSAALTSNGPLLSTVGSYDWAG PPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEWVSTVMEQLKKSKTLFSLMQYSEEF 138 LPVSRQECPRQEQDIVFLIDGSGSISSRNFATMANFVRAVISQFQRPSTQFSLMQFSUKF RIHFTFKEFQNNPNPRSLIKPITQLLGRTHTATGLRKVVRELFNITNGARKNAFKILFLL TDGKKEGDSLDYKDVIPMADAAGIIRYAIGVGLAFONRNSWKELNDIASKPSQEHIFKVE GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR QNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPL PRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLF FNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSTGSCEPI Gaps ; Length 1163; Conservative 142; Mismatches 292; Indels 59.0%; Score 3473; DB 8; 61.0%; Pred. No. 1.4e-281; Query Match Best Local Similarity Matches 689; Conserv Н 61 80 121 198 241 258 438 181 361 421 481 498 ਨੇ d ð qq à qq à Ωp qq g ð 셤 g  $\delta$ g à à ð

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HGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTVGAQGHVLLLRSQ

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960 VRLNQTVIWDRPQVIFSENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDI 1019 1020 PFFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLPGGGAFVRSQTE 1079 919 720 736 780 796 900 959 854 marker gene; inflammatory bowel disease; IBD; FcgammaR IIIa; FcgammaR IIIb; Mig; NRG-2; hexokinase; HM74; REG III; LPAP; Mip-1(beta); L-selectin; EGFL6; IDO; IL-8; CD11c; TLR2; ulcerative colitis; Novel marker gene of inflammatory bowel disease (IBD) comprising base sequence of e.g., Fc gamma R IIIa, Fc gamma R IIIb, Mig, NRG-2, hexokinase 3, HM74, CD11c, TLR2 gene, useful for screening therapeutic 677 LDLALDPGRLSPRATFQETKNRSLSRVRVLGLKAHCENFNLLLPSCVEDSVTPITLRLNF SNLELNAEVWVWNDGEDSYGTTITFSHPAGLSYRYVAEGQKQGQLRSLHLTCDSAPVG--PVLRVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVT YDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNF SLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVG 781 GPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEV SGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRTNKTEF QLELPVKYAVYMVVTSHGVSTKYLNFTAS-ENTSRVMQHQYQVSNLGQRSLPISLVFLVP 915 QLELPVKYAVYTVVSSHEQFTKYLNFSESEEKESHVAMHRYQVNNLGQRDLPVSINFWVP 1080 TKVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMMSE Human inflammatory bowel disease marker - CD11c protein. Ä. ADN02004 standard; protein; 1163 07-AUG-2002; 2002JP-00229705. 07-AUG-2002; 2002JP-00229705 (SUMU ) SUMITOMO SEIYAKU KK. (first entry) WPI; 2004-209124/20. N-PSDB; ADN01990 Crohn's disease JP2004065120-A. Homo sapiens 17-JUN-2004 04-MAR-2004. 557 617 199 721 737 797 855 601 ADN02004; 841 901 ADN02004 à Db à qq ð පු d ð à g à g 8 g ð a à 

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Sequence 1163 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          197
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                                                            disease (IBD)
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                                                       The invention comprises marker genes for inflammatory bowel disease (IE-FogammaR IIIa, FogammaR IIIb, Mig, NRG-2, hexokinase, HM74, REG III, IPAP, Mip-1 (beta), L-selectin, EGFL6, IDO, IL-8, CDILG, and TLR2 genes. The DNA and protein sequences of the invention are useful in the detection and treatment of IBD (e.g. ulcerative colitis and Crohn's disease). The present amino acid sequence represents an IBD marker protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RIHFTFKEFONNPNPRSLIKPITOLLGRTHTATGLRKVVRELFNITNGARKNAFKILFLL
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                                                                                                                                                                                                                            Length 1163;
                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                          ch 58.8%; Score 3459; DB 8; 31 Similarity 60.9%; Pred. No. 2.1e-280; 687; Conservative 142; Mismatches 294;
                               27; 151pp; Japanese
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                               Example; SEQ ID
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                                                                                                                                                                               SQGTWSTSCRINHLIFRGGAQITFLATFDVSPKAVLGDRLLLTANVSSENNTPRTSKTTF
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p150,95 leucocyte adhesion receptor alpha-subunit; hairy cell leukaemia; rhinovirus.
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    1128
                                            TKVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMMSE
                                                                                                                                                                        p150.95 alpha subunit encoded by clone lambdaX47.
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/label= glycosylation site
939. .91.
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1050. .1052
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1108. .1133
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/label= signal peptide
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Similarity 60.9%; Pred. No. 2.1e-280; Conservative 142; Mismatches 294;
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          RNA extracted from phorbol myristate acetate stimulated HL-60 myelomonocytic cells. The library was screened with oligonucleotide probes based on tryptic peptide fragments of p150.95. The sequence can be attached to appropriate control elements and expressed in prokaryotic and eukaryotic cells. The protein can be used to treat or prevent rhinoviral infection because it interacts with ICAM-1 and inhibits cell-virus attachment. It can also be used as an anti-inflammatory agent. See also AAQ066063-4, AAQ066068, AAR07115-8 and AAR07152-6. (Updated on 25-MAR-2003 to correct PR field.)
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                                                                                                                                                                                                                                                                    RLOVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLRQQPQK
                                                                                                                                                                                                                                                                                    GLOVPPEAVNMSLGLSLASTTSPSQLLACGPTVHHECGRNMYLTGLCFLLGPT--QLTQR
                                                                                                                                                                                                                                                                                                                       FPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEWVSTVMEQLKKSKTLFSLMQYSEEF
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                                                                                                                                                                                                                 FNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQELVAANQRGSLYQCDYSTGSCEPI
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                                                                                                                                                                Length 1163;
                                                                                                                                                                58.6%; Score 3450; DB 2; Length 1 60.7%; Pred. No. 1.2e-279; ive 142; Mismatches 296; Indels
from a cDNA library
                                                                                                                                                                                            Conservative 142;
 X47 was isolated
                                                                                                                                                                                Similarity
                                                                                                                                            Sequence 1163 AA;
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This sequence represents a human beta-integrin CDIIc subunit which is used to describe a method for identifying compounds that modulate the interaction of the beta-integrin alpha-d subunit with a binding partner of alpha-d which involves contacting an alpha-d polypeptide with an alpha labelled, in the presence of a test compound, and determining if the compound affects binding between the alpha-d polypeptide and alpha-d binding partner, where the alpha-d polypeptide is alpha-d comprising the cytoplasmic, transmembrane or extracellular domain of alpha-d. Compounds that modulate alpha-d binding could be used to treat diseases such as type-I diabetes, atherosclerosis, multiple sclerosis, asthma, psoriasis, lung inflammation, acute respiratory distress syndrome and rheumatoid arthritis
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labelled alpha-d polypeptide, useful for, e.g. treating type-I diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                   Beta-integrin alpha-d subunit; human; modulator; treatment; psoriasis; type-I diabetes; atherosclerosis; multiple sclerosis; asthma; lung inflammation; acute respiratory distress syndrome; CD11c subunit; rheumatoid arthritis.
                                                                                                                                                                             PFFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLPGQGAFVRSQTE
                QLELPVKYAVYMVVTSHGVSTKYLNFTAS-ENTSRVMQHQYQVSNLGQRSLPISLVFLVP
                                                                                                           VRLNQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDI
SGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRTNKTEF
                                                                                                                                                                                                                                 TKVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMMSE
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94US-00286889.
94US-00362652.
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                                                                    GLQVPPEAVNMSLGLSLASTTSPSQLLACGPTVHHECGRNMYLTGLCFLLGPT--QLTQR
                                                                                                                               121 FPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEWVSTVMEQLKKSKTLFSLMQYSEEF
                                                                                                                                                LPVSROECPROECDIVFLIDGSGSISSRNFATMMNFVRAVISOFORPSTOFSLMOFSNKF
                                                                                                                                                                    181 RIHFTFKEFONNPNPRSLIKPITOLLGRIHTATGLRKVVRELFNITNGARKNAFKILFLL
                                                                                                                                                                                FNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSTGSCEPI
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                                        9
                     Length 1163;
                   Score 3436; DB 2;
Pred. No. 1.8e-278;
3; Mismatches 291;
                                     Conservative 148;
                   58.4%;
                           Similarity
AA;
Sequence 1163
                                   684;
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Integrins are a class of membrane-associated molecules that participate in cellular adhesion. Integrins are made up of an alpha subunit and a common beta subunit. One class of human integrins are restricted to expression in white blood cells and have a common beta subunit: the leukocyte integrins, Leu-CAMB, leukointegrins or beta integrins. Beta integrins have an important role in immune and inflammatory responses. The present protein sequence is the human integrin alpha subunit CDIC. This sequence was used in an alignment to identify a novel beta integrin alpha subunit: alpha d (AAA60014 and AAB07359). The present sequence has subunit: alpha d (AAA60014 and AAB07359). The present sequence has subunit: alpha d (AAA60014 and AAB07359). The present sequence has subunit: alpha d function eag. Type I diabetes, atherosclerosis, multiple consistences syndrome, rheumatoid arthritis and leukocyte adhesion deficiency (IAAD). In addition, anti-alpha d monoclonal antibodies may be used in the inhibition of macrophage infiltration at the site of a central nervous
                                       Use of novel anti-alpha integrin d monoclonal antibodies to inhibit macrophage infiltration and reduce inflammation at central nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; macrophage infiltration inhibition; alpha d integrin; leukocyte integrin; Leu-CAM; leukointegrin; immune response; inflammation; leukocyte adhesion deficiency; LAD; Type I diabetes; atherosclerosis; multiple sclerosis; asthma; psoriasis; beta2 integrin; lung inflammation; acute respiratory distress syndrome; Crohn's disease; rheumatoid arthritis; central nervous system injury; CDllc.
PFFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLPGQGAFVRSQTE
                                                                                                                                             TKVEPFEVPNPLPLIVGSSVGGLLLALITAALYKLGFFKRQYKDMMSE 1128
                                                                                                                                                                                     Length 1163;
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Pred. No. 1.8e-278;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human CD11c protein sequence.
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99US-00350259.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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| 684; Conservative 148; Mismatches 291; Indels 6; Gaps 4;  1 FNLDTENAMTFOENARGEGOSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSTGSCEPI 60 | SAVNWSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLRQDPQK 1 | 1 FPEALLECOPEDSDIAFLIDGSSIIPHDFRRMEWVSTVMBQLKKSKTLFSLMOYSBEF 18 | 181 RIHFTEKEFQNNPNPRSLIKPITQLLGRTHTATGLRKVVRELFNITNGARKNAFKILFLL 240<br> | H 00    | 301 NFEALKTIQNQLREKIFALEGTQTGSSSSFEHEMSQEGFSAAITSNGPLLSTVGSYDWAG 360<br> | 361 GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAFRYQHIGLVAMFR 420<br> | 421 ONTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPL 480 | 481 PRGGRARWCCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLF 540 | 541 HGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTVGAQGHVLLLRSQ 600 | 601 PVLRVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRDFLREGQIQSVVT 660<br> | 661 YDLALDSGRPHSRAVFNETKNSTRROTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNF 720<br> | 721 SLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVG 780<br> | 781 GPREFNVTVTVRNDGEDSYRTQVTFFFELDLSYRKVSTLQNQRSQRSWRLACESASSTEV 840<br>797 SNLEINABVMVWNGEDSYGTTITFSHPAGLSYRYVAEGOXQGQLRSLHLTCCSAPVG 854 | 41 SGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRINKTEF 90  55 SOGTWANTSCRINHLIFPEGGAOTIFLATFDVSPRAVGLBRLLLLANVSSENNIPPRISKTIF 91 | 01 OLELPVKXAVYMVTSHGVSTKXLNFTAS-ENTSRVMQHQYQVSNLGQRSLPISLVFLVP 95 | 60 VRI<br>   <br>75 VEI | 20 PFFG<br>   <br>35 PSFS |
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| Matches<br>Qy   | g & d  |   | Qy 1   | Oy of a | yy du  | oy<br>Db   | , , qa   | oy do  | λ<br>λ<br>ο  | QY<br>Dp   | Sy<br>Sy   | , , , , , , , , , , , , , , , , , , ,                                    | රු සි   | } & £   | od<br>da  | ζς<br>Op                | . Qy 1                    |

Search completed: November 9, 2004, 12:08:19 Job time: 108.25 secs us-09-902-481b-4.rapb

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November 9, 2004, 12:17:49; Search time 97.5 Seconds (without alignments) 4119.157 Million cell updates/sec
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1 FNLDTENAMTFQENARGFGQ.....FKRQYKDMMSEGGPPGAEPQ 1137
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1: cgn2 6/ptodata/2/pubpaa/USO7 PUBCOMB.pep:*
2: cgn2 6/ptodata/2/pubpaa/USO7 PUBCOMB.pep:*
3: cgn2 6/ptodata/2/pubpaa/USO6 NEW PUB.pep:*
4: cgn2 6/ptodata/2/pubpaa/USO6 PUBCOMB.pep:*
5: cgn2 6/ptodata/2/pubpaa/USO6 PUBCOMB.pep:*
6: cgn2 6/ptodata/2/pubpaa/USO7 PUBCOMB.pep:*
7: cgn2 6/ptodata/2/pubpaa/USO9 NEW PUB.pep:*
8: cgn2 6/ptodata/2/pubpaa/USO9 PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1566620 seqs, 353225886 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                            Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           |            | Description     | Sequence 4, Appli | Sequence 3, Appli | Sequence 3, Appli | Sequence 1, Appli | Sequence 3, Appli | Sequence 30, Appl | Sequence 176. App | Sequence 5, Appli | Sequence 6, Appli | Sequence 4. Appli | Sequence 204, App | Sequence 4, Appli | Sequence 4, Appli |
|-----------|------------|-----------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|
| SUMMARIES |            | DI              | US-09-902-481A-4  | US-09-902-481A-3  | US-09-350-259-3   | US-09-902-481A-1  | US-09-891-943-3   | US-10-144-259-30  | US-10-207-655-176 | US-09-902-481A-5  | US-09-902-481A-6  | US-09-945-265-4   | US-10-116-275-204 | US-09-350-259-4   | US-09-891-943-4   |
|           |            | DB              | 10                | 10                | о<br>О            | 10                | 10                | 14                |                   | 10                |                   | ص                 | 14                | σ,                | 10                |
|           |            | Match Length DB | 1137              | 1137              | 1153              | 1153              | 1153              | 1153              | 1153              | 1137              | 1137              | 1152              | 1163              | 1163              | 1163              |
|           | %<br>Query | Match           | 100.0             | 99.5              | 99.5              | 99.5              | 99.5              | 99.5              | 99.5              | 99.4              | 99.3              | 99.2              | 58.8              | 58.4              | 58.4              |
|           |            | Score           | 5884              | 5857              | 5852              | 5852              | 5852              | 5852              | 5852              | 5851              | 5845              | 5836.5            | 3459              | 3436              | 3436              |
|           | Result     | No.             | П                 | 7                 | Э                 | 4                 | Ŋ                 | 9                 | 7                 | 80                | σ                 | 10                | 11                | 12                | 113               |

| 997  | Sequence 99, Appl<br>Sequence 55, Appl<br>Sequence 55, Appl      | i m i           | 37.5             | 9,3  | 4              | H              | ~      | 'n              | N                    | $\ddot{-}$  | 103,             | ö                | 101,     | e 101         |                | 2,             | 103          | 103              | O                | 250                  | $^{\circ}$ | w               | Sequence 35, Appl | 35,           | Sequence 4, Appli  |
|--|--|-----------------|------------------|--|----------------|----------------|--------|-----------------|----------------------|-------------|------------------|------------------|----------|---------------|----------------|----------------|--------------|------------------|------------------|----------------------|------------|-----------------|-------------------|---------------|--------------------|
| 19-350-259-2<br>-09-891-943-2<br>19-350-259-99 | 10 US-09-891-943-99<br>9 US-09-350-259-55<br>10 US-09-891-943-55 | US-09-350-259-5 | 91-943<br>0-259- | 10 US-09-891-943-37<br>9 IIS-09-350-259-46 | US-09-891-943- | 3 US-10-087-19 | Þ      | US-10-261-164-1 | 6 US-10-408-765A-295 | 0-408-765A- | US-09-350-259-10 | 0 US-09-891-943- | 0-259-10 | US-09-891-943 | US-10-177-550- | US-10-173-551- | 9-984-130-10 | US-09-836-353A-1 | US-09-918-715-25 | 17 US-10-474-794-250 | US-10-291  | US-10-291-265-3 | US-09-984-        | -09-836-353A- | 15 US-10-262-839-4 |
| 1161   | 1161<br>1161<br>1161   | 1161            | 1151             | 1151                                       | 1155           | 369            | 1170   | 1170            | 1223                 | 1086        | 494              | 494              | 413      | 413           | 1179           | 1179           | 1151         | 1151             | 1179             | 1179                 | 1188       | 1188            | 1189              | 1189          | 1189               |
| 57.8<br>57.8<br>57.5                           | 57.5<br>24.8<br>8.8  |                 |                  |  | 54.2           |                | 9      | 9               | 25                   | 23          | N                | 20               | 19.      | 19            | 19.4           | 19.            | 18.          | 18.              | 18.6             | •                    |            |                 | 18.4              | 18.4          | 18.4               |
|  | 3385.5<br>3224.5<br>3224.5                                       | 32              | າລ               | 93   |                |                | 1547.5 | m               | 1520                 | 1350.5      | 1229.5           | 1229.5           | 1141.5   | 1141.5        | 1140           | 1140           | 1093.5       | 1093.5           | 93               | m                    | 1092       | 20              | 84                | 1084.5        | 44                 |
| 14<br>15<br>16                                 | 17<br>18<br>19   | 20              | 22               | 23   | 25             | 26             | 27     | 28              | 29                   | 30          | 31               | 32               | 33       | 34            | 35             | 36             | 37           | 38               | 39               | 40                   | 41         |                 | 43                | 44            | 45                 |

APPLICANT: Springer, Timothy
APPLICANT: Shimmack, Motcomu
APPLICANT: Shimmack, Motcomu
APPLICANT: Shimmack, Motcomu
APPLICANT: Shimmack, Motcomu
APPLICANT: Mayo, Stephen
TITLE OF INVENTION: NOVEL PROTRINS WITH INTEGRIN-LIKE ACTIVITY
FILE REFERENCE: A-70586-1/RF7/RMS/RMK
CURRENT APPLICATION NUMBER: US 60/9902, 481A
CURRENT APLICATION NUMBER: US 60/216,600
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 2000-07-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 1137 ; Sequence 4, Application US/09902481A; Publication No. US20030054440A1; GENERAL INFORMATION: ORGANISM: Artificial sequence ; OTHER INFORMATION: synthetic US-09-902-481A-4 US-09-902-481A-4 TYPE: PRT FEATURE:

ALIGNMENTS

1 FNLDTENAMIFOENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSIGSCEPI Gaps Length 1137; 0; Indels DB 10; 0 100.0%; Score 5884; 100.0%; Pred. No. 0; 0; Mismatches Conservative Query Match Best Local Similarity Matches 1137; Conservat

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Query Match
Best Local Similarity 99.5%;
Matches 1131; Conservative
Publication No. US20030054440A1
GENERAL INFORMATION:
                                                                                                                                                         SOFTWARE: PatentIn version 3.1
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                                                                           PRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLF
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                           PPEALRGCPOEDSDIAFLIDGSGSIIPHDFRRMKEWVSTVMEQLKKSKTLFSLMQYSEEF
                                                                                                                                                                          NFEALKTIQNQLREKIFAIEGTQTGSSSSFEHEMSQEGFSAAITSNGPLLSTVGSYDWAG
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Sequence 3, Application US/09902481A

RESULT 2 US-09-902-481A-3

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APPLICANT: Springer, Motomu
APPLICANT: Shifmaoka, Motomu
APPLICANT: Shifman, Julia
APPLICANT: Shifman, Julia
APPLICANT: Mayo, Stephen
TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
FILE REFERENCE: A-70586-1/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/902,481A
CURRENT FILING DATE: 2001-07-09
PRIOR FILING DATE: 2000-07-07
NUMBER: OF SEQ. 10 NOS: 7 Indels 10; 3; DB 3; Mismatches Score 5857; Pred. No. 0; 601 661 70 임

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                                                        RIHFIFKEFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVI
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GENERAL INFORMATION:

APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Michael W.
TITLE OF INVENTION: NO. US20020062008Alel Human 2
FILE REBERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/350,259
CURRENT FILING DATE: 1999-07-08
EARLIER APPLICATION NUMBER: 09/193,043
EARLIER APPLICATION NUMBER: 09/193,43
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-08-05
EARLIER APPLICATION NUMBER: 08/362,652
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1994-10-03
EARLIER FILING DATE: 1997-10-03
EARLIER PLING DATE: 1997-10-03
EARLIER FILING DATE: 1997-10-03
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7; Mismatches
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APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITIE OF INVENTION: NO. US20030077278A1el Hum
TITIE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/891,943
CURRENT FILING DATE: 1998-11-16
PRIOR FILING DATE: 1998-11-16
PRIOR FILING DATE: 1994-08-05
PRIOR PRILING DATE: 1994-12-21
PRIOR FILING DATE: 1994-12-21
PRIOR FILING DATE: 1994-12-21
PRIOR FILING DATE: 1997-10-03
NUMBER: OF SEQ ID NOS: 114
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Best Local Similarity 99.2%;
Matches 1128; Conservative
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ORGANISM: Homo sapiens
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APPLICANT: Shifman, Julia
APPLICANT: Shifman, Julia
APPLICANT: Mayo, Stephen
TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
FILE REFERENCE: A-70586-1/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/902,481A
CURRENT PELLING DATE: 2001-07-09
PRIOR PILLING DATE: 2000-07-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 1153
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Pred. No. 0;
7; Mismatches 2;
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Best Local Similarity 99.2%;
Matches 1128; Conservative
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                                                                                                                                                                                                                                                                                NAME/KEY: mat_peptide;
LOCATION: (17)..()
CTHER INFORMATION:
US-09-902-481A-1
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  FILE REFERENCE: 00786-548001
CURRENT APPLICATION NUMBER: US/10/144,259
CURRENT FILING DATE: 2002-09-04
PRIOR FILING DATE: 2001-01
PRIOR PLING DATE: 2001-01.
PRIOR PLING DATE: 2001-01.
PRIOR FILING DATE: 2000-07-31
NUMBER: OF SEQ ID NOS: 30
SEQ ID NO 30
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Best Local Similarity 99.2
Matches 1128; Conservative
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APPLICANT: Li, Rui
APPLICANT: Xiong, Jian-Ping
TITLE OF INVENTION: VARIANT INTEGRIN POLYPEPTIDES AND USES THEREOF
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Publication No. US20030109691A1
GENERAL INFORMATION:
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publication No. US20030054440A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Springer, Motomu
APPLICANT: Shifman, Unlia
APPLICANT: Shifman, Unlia
APPLICANT: Shifman, Unlia
APPLICANT: Shifman, Unlia
CURRENT RAPLICATION NOWEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
FILE REPERBNEE: A-70586-1/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/902,481A
CURRENT FILING DATE: 2001-07-09
PRIOR PLING DATE: 2001-07-09
PRIOR PLING DATE: 2000-07-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
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GPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEV 856
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                                                             SGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRTNKTEF
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Publication No. US20030118592A1
GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069-40120 NO9-4016.
CURRENT APPLICANTE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
SOFTWARE: Patentin version 3.0
SEQ ID NO 176
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Pred. No. 0;
7; Mismatches
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Best Local Similarity 99.2%;
Matches 1128; Conservative
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ORGANISM: Homo sapiens
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US-10-207-655-176
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Sequence 6, Application US/09902481A
Publication No. US20030054440A1
GENERAL INFORMATION:
APPLICANT: Springer, Timothy
APPLICANT: Shifman, Julia
APPLICANT: Shifman, Julia
APPLICANT: Mayo, Stephen
TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
FILE REFERENCE: A-70586-1/RFT/RMS/RMK
CURRENT PEPLICANTION NUMBER: US/09/902,481A
CURRENT FILING DATE: 2001-07-09
PRIOR PELICATION NUMBER: US 60/216,600
PRIOR FILING DATE: 2000-07-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
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Pred. No. 0;
8; Mismatches
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Best Local Similarity 99.0%;
Matches 1126; Conservative
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; OTHER INFORMATION: synthetic US-09-902-481A-6
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Patent No. US20020123614A1
GENERAL INFORMATION:
APPLICANT: Springer, Timothy A.
APPLICANT: Shimacka, Motomu
APPLICANT: Shringer, Motomu
APPLICANT: Lu, Chafen
TITLE OF INVENTION: MODIFIED POLYPEPTIDES STABILIZED IN A
TITLE OF INVENTION: DESIRED CONFORMATION AND METHODS FOR PROD
FILE REFERENCE: CBN-002CP
CURRENT APPLICATION NUMBER: US/09/945,265
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/229,700
FINGREN FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastsEQ for Windows Version 4.0
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                    677 LDLALDPGRLSPRATFQETKNRSLSRVKVLGLKAHCENFNLLLDSCVEDSVTPITLRLNF
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APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. US20020062008Alel Hum
TITLE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/350, 259
CURRENT FILING DATE: 1999-0-08
EARLIER APPLICATION NUMBER: 09/13,043
EARLIER APPLICATION NUMBER: 08/13,497
EARLIER PLING DATE: 1994-08-05
EARLIER PLING DATE: 1994-08-05
EARLIER PLING DATE: 1994-08-05
EARLIER PLING DATE: 1994-08-05
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EARLIER PLING DATE: 1994-10-03
NUMBER: OF SEQ ID NOS: 114
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Patent No. US20020062008Al
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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APPLICANT: O'Mahony, Daniel J.
APPLICANT: Brayden, David
APPLICANT: Brayden, David
APPLICANT: Brayden, David
APPLICANT: Brayden, Imelda
APPLICANT: Hagins, Lisa
APPLICANT: Lambkin, Inselda
APPLICANT: Hagins, Lisa
TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
CURRENT FILING DATE: 2002-10-04
NUMBER OF SEQ. DE NOS: 349
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Best Local Similarity 60.9%; Pred. No. 6.3e-286;
Matches 687; Conservative 142; Mismatches 294;
                                          Sequence 204, Application US/10116275
Publication No. US20030211476A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn version 3.1
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          CHFTFEEFRRTSNPLSLLASVHQLQCFTYTATATAIQNVVHRLFHASYGARRDAIKILIVI
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RESULT 13 US-09-891-943-4 ; Sequence 4, Application US/09891943

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APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Michael W.
TILE OF INVENTION: No. US20030077278Alel Human 2
FILE REPERENCE: 27866/35004
CURRENT PILING DATE: 2001-06-26
CURRENT FILING DATE: 2001-06-26
PRIOR FILING DATE: 1998-11-16
PRIOR FILING DATE: 1998-11-16
PRIOR PELING DATE: 1998-11-16
PRIOR PELING DATE: 1994-08-05
PRIOR PELING DATE: 1994-08-05
PRIOR PELING DATE: 1994-08-05
PRIOR FILING DATE: 1994-08-05
PRIOR FILING DATE: 1994-08-05
PRIOR FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PALENTIN Ver. 2.0 58.4%; Score 3436; DB 10; llarity 60.6%; Pred. No. 5.9e-284; Conservative 148; Mismatches 291; Publication No. US20030077278A1 GENERAL INFORMATION: ORGANISM: Homo sapiens Best Local Similarity Matches 684; Conserv LENGTH: 1163 TYPE: PRT US-09-891-943-4 241 438 498 541 557 601 661 258 361 121 181 421 481 Query Match  $\delta$ g 8

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US-09-891-943-2
; Sequence 2, Application US/08891943
; Publication No. US20030077278A1
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57.8%; Score 3401; DB 9; Length 1
Best Local Similarity 59.3%; Pred. No. 5.8e-281;
Matches 669; Conservative 167; Mismatches 285; Indels
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US-09-350-259-2
Sequence 2, Application US/09350259
Patent No. US2002062008A1
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
TITLE OF INVENTION: No. US20020062008A1ellER REFERENCE: 27866/3504
CURRENT APPLICATION NOWBER: US/09/350,259
CURRENT APPLICATION NUMBER: US/09/350,259
CURRENT APPLICATION NUMBER: 09/193,043
EARLIER APPLICATION NUMBER: 08/173,497
EARLIER FILING DATE: 1999-1-1-6
EARLIER FILING DATE: 1993-12-23
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-08-05
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EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1997-10-03
NUMBER OF SOE ID NOS: 114
SOFTWARE: PATENTIN VOE: 2.0
SEQ ID NOS: 114
INFORMATE: 1-1
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                                            Human
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. US20030077278A1el Hum
FILE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/891,943
CURRENT FILING DATE: 1998-11-16
PRIOR FILING DATE: 1998-11-16
PRIOR FILING DATE: 1998-12-21
PRIOR FILING DATE: 1994-12-21
PRIOR FILING DATE: 1994-10-03
NUMBER OF SEQ ID NOS: 114
SEGITANG: PATENTION NUMBER: 08/363,652
PRIOR FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 669; Conserv
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Search completed: November 9, 2004, 12:46:53 Job time: 102.5 secs

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17 FNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSTGSCEPI 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/173,497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: No. 5437958 and, Greta E.
REGISTRATION NUMBER: 35,302
REPERENCE/DOCKET NUMBER: 27866/31363
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFEAX: 312-474-6448
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US-08-286-889-3
US-08-485-618-3
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US-08-812-293A-3
US-08-842-293A-3
US-09-193-043-3
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US-09-588-307A-3
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US-08-943-293A-4

US-08-943-363-4

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 GenCore version
Copyright (c) 1993 - 2004
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APPLICANT: Gallatin, W. Michael
APPLICANT: Van Der Vieren, Monica
TITLE OF INVENTION: No. 5437958el Human 2 Integrin Alpha
TITLE OF INVENTION: Subunit
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
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US-08-485-618-2
US-08-362-652-2
US-08-482-293A-2
US-08-943-363-2
US-09-193-043-2
US-09-193-043-2
US-09-185-618-99
US-08-485-618-99
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US-08-482-293A-99
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STREET: 233 S. Wa
CITY: Chicago
STATE: Illinois
COUNTRY: USA
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Alpha Subunit

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317 NFEALKTIONOLREKIFALECTQTGSSSSFEHEMSQEGFSAAITSNGPLLSTVGSYDWAG 376
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                                                                                                                                                                3: Marshall, O'Toole, Gerstein, Murray
233 South Wacker Drive, 6300 Sear Tower
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                                                                                                                                                                                                                                           ZIP: 6666-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
CORRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,889
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION 1435
PRIOR APPLICATION UMBER: US/08/13497
FILING DATE: 23-DEC-1993
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US/08/173,497
FILING DATE: 23-DEC-1993
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Pred. No. 0;
                                                                                                                   Human
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RR: 27866/32168
                                                                               APPLICANT: Gallatin, W. Mich
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5470953e1
NUMBER OF SEQUENCES: 51
                             Sequence 3, Application US/08286889 Patent No. 5470953 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: P38,659 REFERENCE/DOCKET NUMBER: 2786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
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LENGTH: 1153 amino acids
                                                                                                                                                                                                                STATE: Illinois
COUNTRY: United States
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall,
STREET: 233 South Wac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
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Best Local Similarity
Matches 1128; Conserv
                                                                                                                                                                                                  Chicago
RESULT 2
US-08-286-889-3
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                Version
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Pred. No. 0;
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                                                                                                               PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                        US/08/485,618
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                    NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: INFORMATION: 1153 amital Type.
                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                          312-474-6300
                SOFTWARE: Patentin ReleCURRENT APPLICATION DATA:
APPLICATION NUMBER: US/FILING DATE:
CLASSIFICATION: 435
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MOLECULE TYPE: protein
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                     GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR
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233 South Wacker Drive, 6300 Sear Tower
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APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5728533el Human
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08485618
Patent No. 5728533
GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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STREET: 233 South Wacker
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
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US-08-485-618-3
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 REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32391
TELECOWUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEPER: 312-474-0448
TELER: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHRACATERISTICS:
LEUGTH: 1153 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                         Score 5852;
Pred. No. 0;
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Matches 1128; Conservative
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MOLECULE TYPE: protein
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YDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNF
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APPLICANT: Gallatin, W. Michael

APPLICANT: Gallatin, W. Michael

APPLICANT: Gallatin, W. Michael

TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha
NUMBER OF SEQUENCES: 93

CORRESPONDENCE ADDRESS:

ADDRESSEE:
ADSRESSEE: AARSHAll, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PatentIn Release #1.0, Version #1.25
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CLASSIFICATION: 435
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652
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Patent No. 5766850
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MEDIUM TYPE: Floppy disk
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CITY: Chicago
STATE: Illinois.
COUNTRY: United States
ZIP: 60606-6402
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GPREFNVTVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEV 856
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                                                                                                       QLELPVKYAVYMVVTSHGVSTKYLNFTASENTSRVMQHQYQVSNLGQRSLP1SLVFLVPV
                             SGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRTNKTEF
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,672
FILING DATE:
CLASSITCATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 32-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION NUMBER: US 08/362,652
FILING DATE: 15-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REGISTRATION NUMBER: 38,659
REGISTRATION NUMBER: 37,706619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gerstein, Murray
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5817515el Human
NUMBER OF SEQUENCES: 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 60666-6402
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3: Marshall, O'Toole, Ge
233 South Wacker Drive,
                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08605672
Patent No. 5817515
GENERAL INFORMATION:
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TELEPHONE: 312-474-6300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Chicago
STATE: Illinois
COUNTRY: United States
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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STREET: 23
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                                                                                                                                                             HGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTVGAQGHVLLLRSQ
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                                                                  FNLDTENAMTFOENARGFGOSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSTGSCEPI
                                 Gaps
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Length 1153;
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                                 7; Mismatches
 Score 5852;
Pred. No. 0;
                Pred.
   99.5%;
Query Match
Best Local Similarity 99.2
Matches 1128; Conservative
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  TDGEKFGDPLGYEDVI PELDREGVIRYVI GVGDAFRSEKSRQELNTVASKPPRDHVFQIN
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US-08-943-363-3
Sequence 3, Application US/08943363
Patent No. 5837478
GENERAL INFORMATION:
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                                                                              KVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMMSEGGPPGAEPQ 1137
                                                                                                   KVEPFEVPNPLPLIVGSSVGGLILLALITAALYKLGFFKRQYKDWGEGPPGAEPQ 1153
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233 South Wacker Drive, 6300 Sear Tower
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,293A
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                                                                                                                                                                                                                                                                           APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5831029el Human
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                   Sequence 3, Application US/08482293A Patent No. 5831029 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 2786(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
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COUNTRY: United States
ZIP: 60606-6402
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino aci
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; TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-293A-3
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STATE: Illino:
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STREET: 23
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US-08-482-293A-3
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                                                                                                    HGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTWDGLVDLTVGAQGHVLLLRSQ
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                                 GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR
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                                                                                QNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPL
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APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Michael W.
APPLICANT: Jan der Vieren, Monica
TITLE OF INVENTION: No. 6251395e1 Human 2
FILE REFRENCE: 27866/35004
CURRENT FILLING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: 08/173,497
EARLIER FILLING DATE: 1993-12-23
EARLIER FILLING DATE: 1994-08-05
EARLIER FILLING DATE: 1994-08-05
EARLIER FILLING DATE: 1994-12-21
EARLIER FILLING DATE: 1994-12-21
EARLIER FILLING DATE: 1994-12-21
EARLIER FILLING DATE: 1994-12-21
EARLIER FILLING DATE: 1994-12-21
EARLIER FILLING DATE: 1994-12-21
EARLIER FILLING DATE: 1997-10-03
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Patent No. 6251395
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MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: EL BE P. Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN BATA:
APPLICATION NUMBER: US/08/943,363
FILING DATE:
CLASSIFICATION: DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 5-AUG-1994
                                                                                     marshall, O'Toole, Gerstein, Murray 233 South Wacker Drive, 6300 Sear Tower
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Pred. No. 0;
7; Mismatches
APFLICANT: Gallatin, W. Michael
APFLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5837478el Human
NUMBER OF SEQUENCES: 114
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
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Best Local Similarity 99.2%;
Matches 1128; Conservative
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                                                                   CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'T
STREET: 233 South Wacker
CITY: Chicago
STATE: Illinois
CONNTRY: United States
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: sir
TOPOLOGY: linear
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                                              RINQIVIWDRPQVIFSENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDIP 1020
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GENERAL INFORMATION

PATENT No. 6432404

GENERAL INFORMATION

APPLICANT: Gallatin, Michael W.

APPLICANT: Van der Vieren, Monica

TITLE OF INVENTION: No. 6422404el Human Beta-2

FILE REFERENCE: 27866/3666

CURRENT APPLICATION NUMBER: US/09/688,307A

FILE REFERENCE: 200-10-13

PRIOR APPLICATION NUMBER: 09/193,043

PRIOR APPLICATION NUMBER: 09/193,043

PRIOR APPLICATION NUMBER: 09/193,43

PRIOR PILING DATE: 1994-02-22

PRIOR APPLICATION NUMBER: 08/66,889

PRIOR PILING DATE: 1993-12-23

PRIOR PILING DATE: 1994-08-05

PRIOR PILING DATE: 1994-12-21

PRIOR FILING DATE: 1994-12-21

PRIOR FILING DATE: 1994-12-21

PRIOR FILING DATE: 1994-12-21

PRIOR FILING DATE: 1997-10-03

NUMBER OF SEQ ID NOS: 114

SOFTWARE: PATENTIN VET: 2.0
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99.2%; Pred. No. v,
'... 7; Mismatches
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Matches 1128; Conservative
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TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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US-09-688-307A-3
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Pred. No. 0;
7; Mismatches
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SEQ ID NOS: 114
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                                       LENGTH: 1153
TYPE: PRT
CRGANISM: Homo sapiens
US-09-193-043-3
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Best Local Similarity
Matches 1128; Conserv
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Pred. No. 0;
EARLIER FILING DATE: 1994-12-21
EARLIER APPLICATION NUMBER: 08/943,363
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PATENTIN VEY. 2.0
SEQ ID NO 3
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APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 6620915e1 Human 2
FILE REPERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/350,259
CURRENT FILING DATE: 1999-07-08
EARLIER APPLICATION NUMBER: 09/193,043
EARLIER FILING DATE: 1998-11-16
EARLIER FILING DATE: 1993-12-23
EARLIER FILING DATE: 1993-12-23
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER APPLICATION NUMBER: 08/26,585
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US-09-350-259-3
; Sequence 3, Application US/09350259
; Datent No. 6620915
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| 1 FNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSTGSCEPI<br>   | 61 RLOVP<br>                    | 121 FPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEWVSTVMEQLKKSKTLFSLMQYSEEF 18 | 181 RIHFTFKEFQNNPNPRSLIKPITQLLGRTHTATGLRKVVRELFNITNGARKNAFKILFLL 240   | 241   | 301  | 361 GVELYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILENRVQSLVLGAERYQHIGLVAMFR 420<br>              | 421 ONTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCFL 480 | 481 PRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLF 540 | 541 HGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTWDGLVDLTVGAQGHVLLLRSQ 600 | 601 PVLRVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVT 660 | 661 YDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNF 720 [ | 721 SIVGTPLSARGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVG 780 | 781 GPRERNVIVIVRNDGEDSYRIQVIFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEV 840 | 841 SGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMFRTNKTEF 900 | 901 QLELPVKXAVYMVVTSHGVSTKYLNFTASENTSRVMQHQYQVSNLGQRSLPISLVFLVPV 960 | 961 RINQIVIMDRPQVIFSENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDIP 1020 | 1021 FFGIQEBENATLKGNLSFDWYIKTSHNHLLIVSTAEILENDSVFTLLEGGGAFVRSQTET 1080 |
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| <i>₹</i> 8   | \ \text{\delta} \text{\delta}   | VS 40   | 8 &  | ₹ da  | Vy da  | Qy<br>Db  | Sy du  | oy oy  | <i>∂</i> 8   | oy<br>Q  | o da   | <i>₹</i> 8   | <i>\$</i> €  | & da   | QY<br>du   | Q. du   | \$ A   |
| SGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRTNKTEF 916<br>QLELPVKYAVYMVVTSHGVSTKYLNFTASENTSRVMQHQYQVSNLGQRSLPISLVFLVPV 960 | SLPISLVFLVPV 97 IAVCORIQCDIP 10 | QCDIP<br>QCDIP  | FFGIQEEFNATIKGNLSFDWYIKTSHNHLIIVSTAEILFNDSVFTLLPGQGGAFVRSQTET 1096<br>KVEPPEVPNPLPLIVGSSVGGLLLAALITAALYKLGFFKRQYKDMMSEGGPPGAEPQ 1137 | 1097 KVEPFEVPNPLPLIVGSSVGGLLILALITAALYKLGFFKRQYKDMMSEGGPPGAEPQ 1153 | 162A-43<br>43, Application US/08476062A<br>9, 58772A7. | M. Amin<br>CONTROLLING CELLULAR IMMUNE/INFLAMMATORY<br>RESPONSES WITH BETA2 INTEGRINS | Ü.   |  | Vorcein 2 0  |  |  |  | 999  | 000000   |  |   | Score 5821.5; DB 2; Length 1152;<br>Pred. No. 0;                       |

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                                           377 GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR
                                                                                               QNTGMWESNANVKGTQ1GAYFGASLCSVDVDSNGSTDLVL1GAPHYYEQTRGGQVSVCPL
                                                                                                                  437 QNTGMÆSNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPL
                                                                                                                                                                      PRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLF
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Patent No. 1924399

TITLE OF INVENTION: HUMAN CR3a/b HETERODIMERS

TITLE OF INVENTION: HUMAN CR3a/b HETERODIMERS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/78,871

FLING DATE: 16-UNM-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 539,842

FILING DATE: 18-UNM-1990

PRILING DATE: 28-UNM-1990

PRILING DATE: 28-UNM-1996
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                                                                                                       Sequence 43. Application PC/TUS9601314
GENERAL INFORMATION:
APPLICANT: M. Amin Arnaout
TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN
TITLE OF INVENTION: ANTAGONISTS
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 5;
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Pred. No. 0;
7; Mismatches
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.1)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/01314
FILING DATE: 30-JAN-96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/380,167
FILING DATE: 30-JAN-95
ATTORNEY/AGENT INFORMATION:
NAME: JOHN W. Freeman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                00786/267001
                                                                                                                                                                                                                                         E: Fish & Richardson P.C.
225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: John W. Freeman
REGISTRATION NUMBER: 29,066
REPERENCE/DOCKET NUMBER: 0078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 98.9
Matches 1125; Conservative
                                                                                                                                                                                                                                                                           CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
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                                  KVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMMSEGGPPGAEPQ 1137
                                                        KVEPFEVPNPLPLIVGSSVGGLILLALITAALYKLGFFKRQYKDMMSEGGPPGAEPQ 1152
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                                                                                                                                                                                              APPLICANT: Arraout, M. Amin
TITLE OF INVENTION: CONTROLLING CELLULAR IMMUNE/INFLAMMATORY
TITLE OF INVENTION: RESPONSES WITH BETA2 INTEGRINS
CORRESPONDENCE: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1163;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.0
                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: Windows95
SOFTWARE: FestSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,062A
FILING DATE: 07-UN-1995
RIGH APPLICATION NUMBER: 08/216,081
FILING DATE: 21-MAR-1994
APPLICATION NUMBER: 07/537,830
FILING DATE: 04-UAN-1931
APPLICATION NUMBER: 07/539,842
FILING DATE: 18-UIN-1990
APPLICATION NUMBER: 07/539,842
FILING DATE: 18-UIN-1990
APPLICATION NUMBER: 07/212,573
FILING DATE: 28-UIN-1980
APPLICATION NUMBER: 07/212,573
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                                                                                                                                                                                                                                                                                  P. C.
                                                                                                                                              Sequence 44, Application US/08476062A Patent No. 5877275
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                ADDRESSEE: Fish & Richardson STREET: 225 Franklin Street
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TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
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IBM Compatible
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REGISTRATION NUMBER: 29,
REFERENCE/DOCKET NUMBER:
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amino acid
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                             ZIP: 02110-2804
COMPUTER READABLE FORM:
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                                                                                                                  RESULT 14
US-08-476-062A-44
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                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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                                                                                FNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSTGSCEPI
                                                                                                                 RLOVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLRQQPQK
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                 Gaps
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 Pred. No. 0;
7; Mismatches
                 7;
 98.98;
                 Matches 1125; Conservative
Similarity
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Massachusetts

RY: U.S.A. 02110-2804 Boston

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COMPUTER KEADABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: 1BM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION NUMBER: PCT/US96/01314
FILING DATE: 30-JAN-96
                                                                                                                                                                                         FILING DATE: 30-JAN-96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/380,167
FILING DATE: 30-JAN-95
ATTORNEY/ACENT INFORMATION:
NAME: JOHN W. Freeman
    ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                               NAME: John W. Freeman
REGISTRATION NUMBER: 29,066
REPERENCE/DOCKET NUMBER: 007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                    TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino
STRANDEDNESS
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PCT-US96-01314-44
                              CITY: BOS
STATE: Ma
COUNTRY:
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                                                                                                                                                               GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR 420
                                                                                                                                                                                TDGKKEGDSLDYKDVIPMADAAGIIRYAIGVGLAFONRNSWKELNDIASKPSOEHIFKVE
                                                                                                       301 NFEALKTIONOLREKIFALEGTOTGSSSSFEHEMSOEGFSAALTSNGPLLSTVGSYDWAG
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                                                                                                                                             61 RLOVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLRQQPQK
                                                                                                                                                                  80 GLQVPPEAVNMSLGLSLASTITSPSQLLACGPTVHHECGRNMYLTGLCFLLGFT--QLTQR
                                                                                                                                                                                                                   121 FPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEWVSTVMEQLKKSKTLFSLMQYSEEF
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                                                                                                        20 FNLDTEELTAFRVDSAGFGDSVVQYANSWVVVGAPQKITAANQTGGLYQCGYSTGACEPI
                                     Gaps
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Query Match 58.8%; Score 3459; DB 5; Length 1
Best Local Similarity 60.9%; Pred. No. 1.2e-289;
Matches 687; Conservative 142; Mismatches 294; Indels
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Sequence 44, Application PC/TUS9601314
GENERAL INFORMATION:
APPLICANT: M. Amin Arnaout
TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN
TITLE OF INVENTION: ANTAGONISTS
NUMBER OF SQUENCES: 78
CORRESPONDENCE ADDRESS:

RESULT 15 PCT-US96-01314-44

| HGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTVGAQGHVLLLRSQ 600 | 1 YDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNF 720 | GPREFNVTVTVRNDGEDSYRTQVTFFFLDLSYRKVSTLQNQRSQRSWRLACESASSTEV 840 | QLELPVKYAVYMVVTSHGVSTKYLNFTAS-ENTSRVMQHQYQVSNLGQRSLPISLVFLVP 959 | O PFEGIOBEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLFGGGAFVRSQIE 1079 |
|--|--|---|--|---|
| 541 H<br>557 H<br>601 P<br>617 P                                 | 661 Y<br>677 L<br>721 S<br>737 T                                   | •   | 901 09<br>915 Q<br>960 W   | 1020 P<br>1035 P<br>1080 H  |
| \$ 90 \$ 90<br>\$ \$   | 90 OS  | \$ \$ \$ \$ \$  | 20 da 60 da  | oy<br>oy<br>oy  |

Search completed: November 9, 2004, 12:21:04 Job time : 28 secs

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein

Run on:

November 9, 2004, 11:57:37; Search time 27.25 Seconds (without alignments) 4014.622 Million cell updates/sec

5876 1 FNLDTENAMTFQENARGFGQ.....FKRQYKDNMSEGGPPGAEPQ 1137 US-09-902-481B-5 score: Title: Perfect sc Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
3: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| ES        | Description    |        | OCVTP SIL |        | Surface | hocyte fu | , [    |        | alpha 2 | otein hom | integrin alpha-2 | alpha-1 | te-Devor |        | alpha-6 | integrin alpha obs | a i pila |        | aditace | מוועום<br>דיוי | alpha-v | 1 6    |        |        | alpha-6 | alrha-3 | alpha-s | alpha-6 | alpha-8 | 3 1    |
|-----------|----------------|--------|-----------|--------|---------|-----------|--------|--------|---------|-----------|------------------|---------|----------|--------|---------|--------------------|----------|--------|---------|----------------|---------|--------|--------|--------|---------|---------|---------|---------|---------|--------|
| SUMMARIES | ID             | RWHU1B | S00551    | RWHU1C | 803308  | 156126    | A53213 | A45226 | 145914  | S44142    | A33998           | A35854  | A41131   | S06046 | I58409  | T31437             | JC7294   | A35761 | I55534  | 844250         | A36108  | T10050 | A27079 | B36429 | A38457  | A40021  | A27421  | A41543  | S16516  | 840311 |
|           | DB             | -      | ~         | -      | ~       | ~         | 7      | 7      | 7       | 7         | 7                | ~       | ~        | ~      | 2       | 7                  | N        | (7     | 2       | ~              | N       | 7      | 7      | ~      | 7       | 7       | 7       | 7       | 7       | 7      |
|           | Length         | 1153   | 1153      | 1163   | 1170    | 1163      | 1179   | 1151   | 1170    | 1178      | 1181             | 1180    | 1039     | 1038   | 1035    | 1041               | 1054     | 1051   | 1053    | 1053           | 1034    | 1044   | 1049   | 1073   | 1072    | 1051    | 1048    | 1001    | 1044    | 1146   |
| <b>₩</b>  | Query<br>Match | 1 6    | 76.1      |        | 9       |           | •      | 18.8   |         | 18.2      |                  | 18.1    |          | 10.8   |         | 10.5               |          | 9.7    | 9.7     |                | 9.5     | 9.1    | 9.1    |        | ٠       | 9.0     | ٠       | 6.8     | ٠,      | 8.4    |
|           | Score          | ı co   | 4470      | ~      | 1553.5  | 1538.5    | Н      | 1103.5 | 1085    | 1071      | 1068             | 1062    | 663      | 635    | 630     | 614.5              | 579.5    | 572.5  | 567.5   | 555.5          | 542.5   | 535    | 532    | 532    | 3       | 530.5   | 526     | 525.5   | +~1     | 496.5  |
|           | Result<br>No.  | п      | 7         | е      | 4       | Ω.        | 9      | 7      | œ       | o,        | 10               | 11      | 12       | 13     | 14      | 15                 | 16       | 17     | 18      | 19             | 20      | 21     | 22     | 23     | 24      | 25      | 26      | 27      | 28      | 29     |

| position-specific | integrin alpha-2h | integrin althara | glynonrotein TTh | alpha-7 integrin - | leukocyte adhesion | integrin alpha cha | F54F2.1 protein - | integrin alpha v c | hypotherical profe | integrin alpha cha | integrin alpha cha | alveoprotein IIh | integrin alpha cha | alventation TTb = | integrin alpha.1 |
|-------------------|-------------------|------------------|------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|------------------|--------------------|-------------------|------------------|
| 9637              | 434269            | 105950           | A60163           | 1186               | B30892             | 8783               | 4824              | 0571               | 8277               | 9403               | 9433               | 5916             | 1523               | 5917              | 5348             |
| A25               | A34               | JCF              | A60              | 16                 | B3                 | 53                 | S4                | 86                 | \$2                | Ţ                  | T.O.               | 136              | 118                | Ë                 | A5               |
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| H<br>C |   |
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cell surface glycoprotein CD11b precursor [validated] - human N;Alternate names: complement receptor type 3 alpha chain; leukocyte adhesion protein Me eukocyte integrin alpha chain; neutrophil adherence receptor alpham chain

C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 31.Dec.1992 #sequence revision 31.Dec.1992 #text\_change 09-Jul-2004
C;Date: 31.Dec.1992 #sequence revision 31.Dec.1992 #text\_change 09-Jul-2004
C;Accession: A31108; A28915; A28015; A18001; I52567
R;Corbi, A.L.; Kishimoto, T.K.; Miller, L.J.; Springer, T.A.
J. Biol. Chem. 263, 12403-12411, 1988
A;Title: The human leukocyte adhesion glycoprotein Mac-1 (complement receptor type 3,

A; Reference number: A31108; MUID:88315033; PMID:2457584

C

A;Accession: A31108
A;Molecule type: mRNA
A;Residues: 1-1153 <COR.
A;Residues: 1-1153 <COR.
A;COSS-references: UNIPROT:P11215; GB:J03925; NID:g187284; PIDN:AAA59544.1; PID:g307148
A;Cross-references: UNIPROT:P11215; GB:J03925; NID:g187284; PIDN:AAA59544.1; PID:g307148
A;Note: part of this sequence was confirmed by protein sequencing
B;Arnaout, M.A.; Gupta, S.K.; Pierce, M.W.; Tenen, D.G.
A;Title: Amino acid sequence of the alpha subunit of human leukocyte adhesion receptor N
A;Reference number: A28915; MUID:88257215; PMID:2454931

A, Molecule type: mRNA
A, Residues: 1-499,501-965, 'P', 967-1153 < ARN>
A, Rolecule type: mRNA
A, Residues: 1-499,501-965, 'P', 967-1153 < ARN>
A, Cross-references: GB:M1964; GB:M03270; GB:M19664; GB:X07421; NID:g186935; PIDN:AAA594
A, Note: the authors translated the codon TAC for residue 1129 as Thr
A, Note: part of this sequence, including the amino end of the mature protein, was confir
B, Shelley, C.S.; Arnaout, M.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 10525-10529, 10529
A, Title: The promoter of the CD11b gene directs myeloid-specific and developmentally reg
A, Reference number: A41600; MUID:92073318; PMID:1683702
A, Residues: 1-9 < SHE>
A, Cross-references: GB:M76724; NID:g180018; PIDN:AAA58410.1; PID:g553215
B, Arnaout, M.A.; Remold-O'Donnell, E.; Pierce, M.W.; Harris, P.; Tenen, D.G.
Proc. Natl. Acad. Sci. U.S.A. 85, 2776-2780, 1988
A, Title: Molecular cloning of the alpha-subunit of human and guinea pig leukocyte adhesi

A; Accession: A30892

A; Molecule type: mRNA A; Residues: 917-1042 <AR2>

A;Cross-references: GB:M18044
R;Hickstein, D.D.; Hickey, M.J.; Ozols, J.; Baker, D.M.; Back, A.L.; Roth, G.J.
Proc. Natl. Acad. Sci. U.S.A. 86, 287-261, 1989
A;Title: CDNA sequence for the alpham subunit of the human neutrophil adherence receptor A;Reference number: A33218; MUID:89098893; PMID:2563162

A;Molecule type: mRNA A;Residues: 9-1153 <HIC> A;Cross-references: GB:J04145; NID:g189068; PIDN:AAA59903.1; PID:g386975

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leukocyte surface glycoprotein Mac-1 alpha chain precursor - mouse
NyAlternate names: complement-3 receptor alpha chain
Sispedies: Mus musculus (house mouse)
C;Becession: S00551; 159078
C;Accession: S00551; 159078
C;Accession: S00551; 159078
A;Title: Amino acid sequence of the murine Mac-1 alpha chain reveals homology with the A;Title: Amino acid sequence of the murine Mac-1 alpha chain reveals homology with the A;Accession: S00551; MUID:88312584; PMID:3044779
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: UNIPROT:P05555; EMBL:X07640; NID:952982; PIDN:CAA30479-1; PID:95298
A;Cross-references: UNIPROT:P05555; EMBL:X07640; NID:952982; PIDN:CAA30479-1; PID:95298
A;Note: the authors translated the codon CAC for residue 569 as Gln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLPGQGAFVRSQTET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1037 FFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLPGQGAFVRSQTET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEV
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                                                                                                                                                   ONTGMMESNANVKGTQ1GAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPL
                                                                                                                                                                                                                                                                                                                                         PRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLF
                                                                                                                                                                                                                                                                                                                                                                          617 PVLRVKAIMEFNPREVARNVPECNDQVVKGKBAGEVRVCLHVQKSTRDRLREGQIQSVVT
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                                               317 NFEALKTIQNQLREKIFALEGTQTGSSSSFEHEMSQEGFSAAITSNGPLLSTVGSYDWAG
                                                                                                                                                                                                                                  ONIGMWESNANVKGIQIGAYFGASLCSVDVDSNGSIDLVLIGAPHYYEQIRGGQVSVCPL
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     NFEALKTIQNQLREKIFAIEGTQTGSSSSFEHEMSQEGFSAAITSNGPLLSTVGSYDWAG
                                                                                                                  GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR
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A;Note: part of this sequence was confirmed by protein sequencing
R;Fleming, J.C.; Pahl, H.L.; Gonzalez, D.A.; Smith, T.F.; Tenen, D.G.
J. Immunol. 150, 480-490, 1993
A;Title: Structural analysis of the CD11b gene and phylogenetic analysis of the alpha-in nduring evolution.
A;Reference number: A46526; MUID:93123748; PMID:8419480
A;Accession: A46526
A;Accession: A46526
A;Accessor of compared with conceptual translation
A;Nolecule type: DNA
A;Residues: 1-499;501-1153 cFLE>
A;Cross-references: GB:55227; NID:9263047; PIDN:AAB24821.1; PID:9263049
A;Note: sequence extracted from NCBI backbone (NCBIP:121963)
A;Note: sequence extracted from NCBI backbone (NCBIP:121963)
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A;Note: sequence extracted from NCBI backbone (NCBIP:121963)
A;Note: sequence extracted from NCBI backbone (NCBIP:131963)
A;Note: sequence extracted from NCBI backbone (NCBIP:131963)
A;Reference number: A50064; MUID:8706671; PMID:353202
A;Residues: 17-31 cPIE>
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A,Gene: GDB:ITGAM; CR3A
A,Gene: GDB:ITGAM; CR3A
A,Gene: GDB:ITGAM; CR3A
A,Gene: GDB:ITGAM; CR3A
A,Gene: GDB:ITGAM; CR3A
A,Gene: GDB:ITGAM; CR3A
A,Gene: GDB:ITGAM; CR3A
A,Gene: GDB:ITGAM; CR3A
A,Gene: GDB:ITGAM; CR3A
A,Map position: 16pil.2-16pil.2
A,Note: promoter contains a GATA motif and two Spl consensus binding sites
A,Note: promoter contains a GATA motif and two Spl consensus binding sites
C,Superfamily: cell surface glycoprotein CDlb; von Willebrand factor type A repeat homo
C,Geywords: alternative splicing; calcium; cell adhesion; glycoprotein; heterodimer; mag
F;1-16/Domain: signal sequence #status predicted <8IG>
F;17-1108/Domain: extracellular #status predicted <8IG>
F;17-1108/Domain: von Willebrand factor type A repeat homology <WAZ>
F;465-478/Region: calcium/magnesium binding #status predicted
F;530-538/Region: calcium/magnesium binding #status predicted
F;530-538/Region: calcium/magnesium binding #status predicted
F;1109-1134/Domain: transmembrane #status predicted <ITM>
F;11135-1153/Domain: intracellular #status predicted <ITM>
F;185-41031,469,693,697,735,802,881,901,912,941,947,979,994,1022,1045,1051,1076/Binding
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Best Local Similarity 99.3
Matches 1129; Conservative
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R;Sastre, L.; Roman, J.M.; Teplow, D.B.; Dreyer, W.J.; Gee, C.E.; Larson, R.S.; Roberts, Proc. Natl. Acad. Sci. U.S.A. 83, 5644-5648, 1986
A;Title: A partial genomic DNA clone for the alpha subunit of the mouse complement recep A;Reference number: IS9078; MUID:86287312; PMID:2942940
A;Accession: IS9078; MUID:86287312; PMID:2942940
A;Accession: IS9078; MUID:86287312; PMID:2942940
A;Accession: IS9078
A;Accession: IS9078
A;Graus: pre-liminary; translated from GB/EMBL/DDBJ
A;Residues: 11-44 «RES»
A;Gross-references: GB:M14293; NID:g198993; PIDN:AAA39484.1; PID:g554193
C;Gene: Mac.1
C;Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homo C;Feywords: cell adhession; glycoprotein, transmembrane protein
F;1-16/Domain: signal sequence #status predicted <SIG.
F;17-1153/Product: leukocyte surface glycoprotein Mac.1
F;148-318/Domain: von Willebrand factor type A repeat homology <VWA2>
F;1106-1129/Domain: transmembrane #status predicted <TMM>
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Gibter 31.Pec-1929 #sequence revision 31-Dec-1932 #text_change 09-Uul-2004
Giocession: A36584, A35543; SO0864
Giocession: A36584, A35543; SO0864
Giocession: A36584, A35543; SO0864
A; Recent caretum
A; Contents: erratum
A; Accession: A36584
A; Molecule erratum
A; Accession: A36584
A; Molecule type: DNA
A; Residues: 1-163 - CCAS
A; Contents: erratum
A; Rocession: A36584
A; Molecule type: DNA
A; Reference number: A35543
A; Molecule type: DNA
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A; Reference number: A35543
A; Molecule type: DNA
A; Reference number: A35543
A; Molecule type: DNA
A; Reference number: S00864; MUD: 9015396; PMID: 332697
A; Title: CDNA CIOINING and complete primary structure of the alpha subunit of a leukocyte
A; Title: CDNA CIOINING and complete primary structure of the alpha subunit of a leukocyte
A; Title: CDNA CIOINING and complete primary structure of the alpha subunit of a leukocyte
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A; Title: CDNA CIOINING and complete primary structure of the alpha subunit of a leukocyte
A; Title: CDNA CIOINING and complete primary structure of the alpha subunit of a leukocyte
A; Common beta chain (CDIB) forms a heterodimer with CDIB to form Mac-1 on my
A; Genetics:
C; CSUPPErfamily: cell surface divcoprotein CDIB; von Willebrand factor type A; Tepeat home
C; Reperence: CBN: TGNA; CDIC
C; Reported: CElling cell aniface divcoprotein CDIB; von Willebrand factor type A; Tepeat home
C; Reported: Celling cell aniface divcoprotein CDIB; Von Willebrand factor type A; Tepeat home
C; Reported: Celling cell aniface divcoprotein CDIB; Title: CDNA
C; Molecule type: MOLECULE CELL S
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                                                916 FQLELPVKYAIYMIVTSDESSIRYLNFTASEMTSKVIQHQYQFNNLGQRSLPVSVVFWIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alternate names: leukocyte adhesion receptor p150,95 alpha chain Species: Homo sapiens (man)
Date: 31-Dec-1992 #sequence revision 31-Dec-1992 #text_change 09-Jul-2004
    GPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRL-ACESASSTE
                                                                                                                                                                                                                             GHGALKSTIWNINHPIFPANSEVIFNVIFDVDSHASFGNKLLLKAIVASENNMSRIHKIK
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                                                                                                  RLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLRQQPQK 120
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                                                                             FNLDTEELTAFRVDSAGFGDSVVQYANSWVVVGAPQKITAANQTGGLYQCGYSTGACEPI
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                            Gaps
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   Length 1163;
                            Indels
   59.2%; Score 3479; DB 1;
ilarity 61.1%; Pred. No. 9.3e-234;
Conservative 141; Mismatches 292;
Query Match
Best Local Similarity
Matches 690; Conserv
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A; Residues: 1-20 < COR>
A; Molecule type: DNA
A; Residues: 1-20 < COR>
A; Note: sequence extracted from NCBI backbone (NCBIN:130862, NCBIP:130863)
R; Shelley, C.S.; Farokhad, O.C.; Arnaout, M.A.
R; Shelley, C.S.; Farokhad, O.C.; Arnaout, M.A.
Proc. Natl. Acad. Sci. U.S.A. 90, 5344-5368, 1993
A; Title: Identification of cell-specific and developmentally regulated nuclear factors A; Reference number: A47565, MUID:93281759; PMID:8099450
A; Rocession: A47565
A; Rocession: A47565
A; Residues: 1-20 < SHE
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PFFGIQEBFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLPGQGAFVRSQTE 1079
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A,Rolecule type: MRNA
A,Residues: 1-1170 *LAR>
A,Residues: 1-1170 *LAR>
A,Cross-references: UNIPROT:P20701; UNIPROT:Q9UBC8; EMBL:Y00796; NID:g31421; 1A,Cross-references: UNIPROT:P20701; UNIPROT:Q9UBC8; EMBL:Y00796; NID:g31421; 1A,Cross-references: UNIPROT:P20701; UNIPROT:Q9UBC8; EMBL:Y00796; NID:g31421; 1A,Cross-reference management R.A.; Hickstein, D.D.
Proc: Natl. Acad. Sci. U.S.A. 90, 4221-4225, 1993
A,Title: Description of the leukocyte function-associated antigen 1 (LFA-1 or A,Reference number: A47458; MUID:93248261; PMID:8097887
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                                                1 FNLDTENAMTFQ---ENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSTGSCE
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26.4%; Score 1553.5;
Best Local Similarity 34.7%; Pred. No. 1.5e-
Metches 407; Conservative 206; Mismatches
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LQGRPGFQECIKG----NVDLVFLFDGSMSLQPDEFQKILDFMKDVMKKLSNTSYQFAAV 196
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| KVLIIITDGE--ATDSGNIDAAKD-----IIRYIIGIGKHFQTKESQETLHKFASKPASE
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                   QYSBEFRIHFTFKEFQNNPNPRSLIKPITQLLGRTHTATGIRKVVRELFNITNGARKNAF
                                 KILILITDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTVASKPPRD
                                                                                                HVFQINNFEALKTIONQLREKIFALEGTQTGSSSSFEHEMSQEGFSAAITSNGPLLSTVG
                                                                                                                                       SYDWAGGVF-LYTSKEKSTFINMTRVDSDMNDAYLGYAAA-IILRNRVQSLVLGAPRYQH
                                                                                                                                                                              IGLVAMFR--QNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQT
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lymphocyte fuction-associated molecule-1-alpha - mouse
C;Species: Mus musculus (house mouse)
C;Becies: Mus musculus (house mouse)
C;Becies: Je-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: 156126
R;Kaufmann, Y.; Tseng, B.; Springer, T.A.
J. Tamin 1 147, 369-374, 1991
A;Title: Cloning of the murine lymphocyte function-associated molecule-1 alpha-subunit
A;Reference number: 156126; MuID:91268576; PMID:2051027
A;Accession: 156126
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residus: 1-1163 <RES>
A;Residues: 1-1163 <RES>
A;Residues: 1-1163 <RES>
A;Gross-references: UNIPROT:P24063; GB:M60778; NID:9198785; PIDN:AAA39426.1; PID:919878
C;Genetics:
A;Gene: LFA-1
C;Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat hom
F;151-315/Domain: von Willebrand factor type A repeat homology <WWAI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                292 PRDHVFQINNFEALKTIQNQLREKIFAIEGTQTGSSSSFEHEMSQEGFSAALTSNGPLLS
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RESULT 156126

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Cipecies: Homo sapiens (man) (fragment)
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cipecies: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
Cipecession: A45226
Ribriesewitz, R.; Epstein, M.R.; Marcantonio, B.E.
J. Baiol. Chem. 268, 2989-2996, 1993
A;Title: Expression of native and truncated forms of the human integrin alpha 1 subuni
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                                                                        SSHGSRRKASKVMVVLTDGGIFEDPLNLTTVINSPKMQGVERFALGVGEBFKSARTAREL 354
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                                                 NTVASKPPRDHVFQINNFEALKTIQNQLREKIFAIEGTQTGSSSSFEHEMSQEGFSAALT
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C;Species: Homo sapiens (man)
C;Date: 19-Oct-1995 #sequence_revision 31-Mar-2001 #text_change 09-Jul-2004
C;Date: 19-Oct-1995 #sequence_revision 31-Mar-2001 #text_change 09-Jul-2004
C;Accession: A53213
N;Daw, S.K.; Cepek, K.L.; Murphy, E.A.; Russell, G.J.; Brenner, M.B.; Parker, C.M.
J. Biol. Chem. 269, 6016-6025, 1994
A;Aitelernce number: A53213; MUID:94164962; PMID:8119947
A;Accession: A53213
A;Accession: A53213
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Acsiones: 1-1179 <SHA>
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                                                                                                                                                                                                                                                                                                            E-RLPSHSDFLABLRKAPVVNCSIAVCQRIQCDIPFFGIQEEFNATLKGNLSFDWYIKTS 1045
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                                                                                                                                                                                                                                         935 VMQHQYQVSNLGQRSLPISLVFLVPVRLNQTVIWDRPQ----VTFSENLSS----TCHTK 986
                                                                                                                                                                                                                                                             943 QVQHVYQV-----RIQPSAYDHNMPT-LEALVGVPRPHSEDLITYTWSVQTDPLVTCHSE 996
                                                                                                                                                                                                      WEDFVELNGTVHCENENSSLQEDNSAATHIPVLYPVNILTKEQENSTLYISFTPKGPKTQ 942
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                                                                                                                                                                                                                                                                                                                                                                               HNHLLIVSTABILFNDSVFTLLPGQGAFVRSQTETKVEPFEVPNPLPLIVGSSVGGLLLL
                              DDLSITFSFMSLDCLVVGGP------REFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKV
                                                            775 ANLTLSSPARS-----GPLRLMSSASLAVEWTLSNSGEDAYWVRLDLDFPRGLSFRKV
                                                                                                    STLONORSORSWRLACESASSTEVSGAL-KSTSCSINHPIFPENSEVTFNITFDVDSKAS
                                                                                                                                 BMLQ---PHSRMPVSCBEL--TEGSSLLTKTLKCNVSSPIFKAGQEVSLQVMFNTLLNSS
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C;Superfamily: cell surface glycoprotein CD11b; von Willebrand
F;199-371/Domain: von Willebrand factor type A repeat homology
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Best Local Similarity 29.1%; Pred. No. 1.2e-71;
Matches 342; Conservative 214; Mismatches 449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALITAALYKLGFFKRQYKDMM-SEGGPPGAEP 1136
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A;Gene: GDB:ITGAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SRAVENET -----KNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNFSLVGT 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SRSFFSGTQERKVQRNITVRKSEC----TKHSFYMLDKHDFQDSVR---IILDFNLT-D 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FNVTVTVRNDGEDSYRIQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEVSGAL 844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              853
                                                                                                                                                                                                                                                   FNVDVKNSMTFSGPVEDMFGYTVQQYENEEGKWVLIGSPLVGQPKNRTGDVYKCPVGRGE
                                                                                                                                                                                                                      FNLDTENAMTFQENARG-FGQSVVQL---QGSRVVVGAPQEIVAANQRGSLYQCDYSTGS
                                                                                                                                                                                                                                                                                CEP-IRLOVPVEA------VNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TEARGARRGVKKVWVIVIDGESH-DNHRLKKVIQDCEDENIQRFSIAILGSYNRGNLSTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AIILRNRVQSL-VLGAPRYQHIGLVAMFRQNTGMWESNANVKGTQIGAYFGASLCSVDVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GEQGQPWG-RFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLFHGTSGSGISPSHSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVGGPRE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PENG-----PVLDDSLPNSVHEYIPPAKDCGNKEKCISDLSLHVATTEKDLLIVRSQNDK
                                                                                                                                   < VWA1>
                                                                                                                                                                                               195;
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A, Reference number: A45226, MUID:93155124; PMID:8428973
A, Accession: A45226
A, Status: preliminary; not compared with conceptual translation
A, Molecule type: mRNA
A, Residues: 1-1151 (-8RL)
A, Cross-references: UNIPROT:P56199
A, Cross-references: UNIPROT: P56199
A, Experimental source: hepatcoblastoma cell line HepG2
A, Note: sequence extracted from NCBI backbone (NCBIP:124326)
F,142-317/Domain: von Willebrand factor type A repeat homology
                                                                                                                                                        Query Match 18.8%; Score 1103.5; DB 2; Length Best Local Similarity 27.8%; Pred. No. 3.3e-68; Matches 344; Conservative 212; Mismatches 486; Indels
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integrin alpha 2 subunit - bovine (fragment)
(5)Species: Bos primigenius taurus (cattle)
(5)Date: 16-Aug-1996 #sequence\_revision 16-Aug-1996 #text\_change 09-Jul-2004
(5)Accession: 145914
(6)Accession: 145914
(7) R:Kamata, T.; Puzon, W.; Takada, Y.
(7) Biol. Chem. 269, 9659-9663, 1994
(7) Title: 1dentification of putative ligand binding sites within the I-domain of integrin A)Reference number: A54402; MUID:94193647; PMID:7511592
(8)Accession: 145914
(8)Accession: preliminary; translated from GB/EMBL/DDBJ A,Molecule,type: mRNA A;Residues: 1-1170 «KAM» A;Cross-references: UNIPROT:P53710; CB:L25886; NID:g439695; PIDN:AAB59255.1; PID:g439696 F;161-336/Domain: von Willebrand factor type A repeat homology «VWA2» -- EFNATLK 1033 973 KLSISFPNMTSNGYPVLYPTGLSS-----SENANCRPHIFEDPFSINSGKKMTT 1021 1034 GNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLPGQGAFVRSQTETKVEPFEVPNPLPL 1093 950 972 991 ---OKRELAIQISKDGLÞGRVÞL 1114 47 79 TTCEKLNLÓTSTSMSNVTEMKTNMSLGLTLTRNVGTGGFLTCGPLWAQQCGSQYYTTGVC 138 107 108 FLFGSNLRQQPQKFPEALRGCPQEDSDIAFLVDGSGSIIPHDFRRAKEFISTVMEQLK-- 165 SDVSPDF-QLRTSFAPAVQTCP-SFIDVVVVCDESNSIYPWD--AVKNFLEKFVQGLDIG 194 310 336 KSKTLFSLMQYSEEFRIHFTFKEFQNNPNPRSLIKPITQLL----GRTHTATGIRKVVRE 221 222 LFNITNGARKNAFKILILITDGEKFGDPLGYEDVIPEADREGVIRYVIGV-----GDAFR 276 EGFSAAIT--SNGPLLSTVGSYDWAGGVFLYTSKEKSTFINMT--RVDSDMN-DAYLGYA 391 78 251 369 KSTSCSINHPIFPENSEVTFNITFDVDSKASLGN-KLLLKANVTSENNMPRTNKTEFQLE HNITCKVGYPFLRRGEMVTFKILFQFNTSYLMENVTIYLSATSDSEEPPETLSDNVVNIS ---RLPS :| |:: :::|: 1022 STD---HLKRGTILDCNTCKFATITCNLTSSDISQVNVSLILWKPTFIKSYFSSLNLTIR 1 FNLDTENAMTFQ-ENARGFGQSVVQL---QGSRVVVGAPQEIVAANQRGSLYQC--DYST GSCEPIRLQ-----VPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLC :: | | | | | :::::||| | | : | | : | | | ANSTAAGGREGATKVMVVVTDGESH-DGSKLKAVIDQCNKDNILRFGIAVLGYLNRNALD ::: :|: || | | | | ::: TKNLIKEIKAIASIPTERHFFNVSDEADLLEKAGTIGEQIFSIEGTVQG-GDNFQMEMSÖ SEKSRQELNTVASKPPRDHVFQINNFEALKTIQNQLREKIFAIEGTQTGSSSSFEHEMSQ Indels 168; Length 1170; PISLVF------LVPVRLNQTVIWDRPQVTFSENLSSTCHTKE----IVGSSVGGLLLLALITAALYKLGFFKRQYKDMMSE 1128 LPVKYAVYMVVTSHGVSTKYLNFTASENTSRVMQHQYQVSN. Query Match
18.5%; Score 1085; DB 2;
Best Local Similarity 27.6%; Pred. No. 6.6e-67;
Matches 335; Conservative 217; Mismatches 495; 992 HSDFLAELRKAPVVNCSIAVCORIQCDIPFFGIQE---GEL-----RSENASLVLSSSN--854 951 845 904 1094 991 195 277 311 337 d ઠે g qq ð à g ò g à ð 8 셤 임 à ð ò g 8 Db à 임  $\delta$ Db à

| qq                               | 370 VGFSAEYSPQNNILMLGAVGAYDWSGTVVQKTPHGHLIFSKQAFBQILQDRNHSSYLGYS 429   | A;Cross-reference<br>F;169-344/Domain: | -references: UNIPROT<br>44/Domain: von Wille |
|----------------------------------|--|--|--|
| Ολ                               | 2 AAIILRNRVQSLVLGAPRYQHIGLVAMFRQNTGMWESNANVKGTQIGAYFGASL   | Query Match                            | ch<br>1 Similarity 2                         |
| QQ                               |  | Matches                                | 2;   |
| Oy.                              | 6 CSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPLPRGQRARWQCDAVLYGEQGQPWG   | ò                                      | 1 FNLDTENAMTFQ-                              |
| qq                               |  | qa                                     | 27 YNVGLPGAKIFSG                             |
| \(\delta \)                      | 504 RFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLFHGTSGSGISPSH9QRIAGSKL 561   | δy                                     |  |
| 3 8                              |  |  |  |
| 2 원                              |  | Oy i                                   | 108 FLFGSNLKQQPQ-<br>147SDWSDNFOF            |
| δy                               | 622 ECNDQVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVTYDLALDSGRPHSRAVFN 677   |  |  |
| ФФ                               | 659 NKNAEIKLKLCFSAKFRPINQNAQVALVYNITIDEDQFSSRVISRGLFK 707  |  | : : <br>  Soo DIGPKKTQVALIQ                  |
| ò                                | 678 ETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDFVSPIVLRLNFSLVGTPLSAFGNL 733   |  | 222 LFNITNGARKNAF                            |
| qq                               | 708 ENNERCLOKTMIVSQAQRCSBYITHIQEPSDIISPLNLCMNISLENPGT 756  | <b>q</b> 0                             | :  :     <br>260 AYSQTSGGRPGAT               |
| ò                                | 78   | <br>                                   | 277 SEKSRQELNTVAS                            |
| qq                               |  | ପ୍ର                                    | 319 TKNLIKEIKAIAS                            |
| ολ                               | 0 TVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASST-EVSGALKSTS ::  | λō                                     | 337 EGFSAAITSNG                              |
| QQ                               |  | qq                                     | 378 VGFSADYAPQNDI                            |
| ζ                                | 9 CSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMFRTNKTEFQLELPVKY   | δλ                                     | 392 AAIILRNRVQSLV                            |
| qq                               | SQEENMADINSVINDALLI  | qa                                     | 438 VAAISTEDGVHFV                            |
| රු ස්                            | 909 AVYMVVTSHGVSTKYLNFTASENTSRVMQHQYQVSNLGQRSLFISLVFLV 958  0.0 ADATH DE THE THE THE THE THE THE THE THE THE TH  | δλ                                     | 448 VDVDSNGSTDLVI                            |
| 2 6                              | PERMITTED NOTATION OF THE PROPERTY OF THE PROP | qq                                     | 495 VDVDKDTITDVLI                            |
| à i                              | PVKLNQIV MUKPQVIFSENLESSICAIANE  | δλ                                     | 506 GAALTVLGDVNGD                            |
| qq                               | SVIIHIPQTIKDKNPLMILIGVHIDQAGDISCEABINFLATGGISSSVSFASEN   | ДС                                     | 552 GSALAALSDINM                             |
| yo da                            | 999 I.RKAPVYNCSIA/CORIOODIPFFGIOBEFNATLKGNUSFDWAIKISHUHLLIVSTATEL 105/<br>   |  | 565 -LQYFGQSLSGGC                            |
| à                                |  |  | 611 HLQFFGRSLDGIC                            |
| ΩD                               | :   : : : : :  | දි සි                                  |  |
| δ                                | 1111 ALYKLGFPKRQYKDM 1125  | à à                                    |  |
| Dp                               | 1141 ILWKLGFFKKYEKM 1155   | Db                                     | ::  :<br>718 SERFLQKNMVVNI                   |
| RESULT                           | 6  | ον                                     | 738 AEDAQRLFTALF                             |
| S44142<br>VLA-2 p                | rotein homolog - mouse   | ପ୍ପ                                    | 769 EAYSETVKVFSII                            |
| C;Spec:<br>C;Date<br>C:Acces     | ange 09-Jul-2004   | λō                                     |  |
| R, Edelı                         | dan, J.M.; Chan, B.M.; Uniyal, S.; Onodera, H.; Wang, D.Z.; Damjanovich, L.; Latze   | QQ                                     | 824 VILKNRGESAYN                             |
| A; Desc<br>A; Refe               | Submitted to the EMBL Data Library, January 1997. A)Description: The mouse VLA-2 homologue supports collagen and laminin adhesion but not A)Reference number: S44142   | Qy                                     | 848 SCSINHPIFPEN :   : :   872 TCDVGYPALKSE  |
| A; Status: pro<br>A; Molecule to |  | δλ                                     | 906 UKYAVYMVVISH                             |
| +23414 .                         | •  |  |  |

T:062469; EMBL:229987; NID:g473098; PIDN:CAA82877.1; PID:g4730 ebrand factor type A repeat homology <VWA2> --SLPISLV 955 | |:|: NSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRTNKTE--FQLELP 905 099 768 FPFEKNCGNDNICQDDLSI-----TFSFMSLDCLVVGGPREFNVT 788 823 NTVVLABESENLFF-----ASFSMPVDGTEVTCEVGSSQKSV 871 447 494 VLIGAPHYYEQTR--GGQVSVCPLPRGQRARWQCDAVLYGEQGQPWGRF 505 564 PODLITMDGLVDLTVGAQGHVLLLRSQPVLRVKAIMEFNPREVARNVFEC 623 619 717 GLTQTCET--LKLQLPNCIEDPVSPIVLRLNFSLVGTPLSAFGNLRPVL 737 FKILILITDGEKFGDPLGYEDVIPEADREGVIRYVIGV-----GDAFR 276 ASKPPRDHVFQINNFEALKTIQNQLREKIFALEGTQTGSSSSFEHEMSQ 336 437 551 ----VPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLC 107 QYSEEFRIHFIFKEFQNNPNPRSLIKPITQLLG-RTHTATGIRKVVRE 221 GPLLSTVGSYDWAGGVFLYTSKEKSTFINMT--RVDSDWN-DAYLGYA 391 ---KFPEALRGCPQEDSDIAFLVDGSGSIIPHDFRRAKEFISTVMEQL 164 RTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASST-EVSGALKST NEVQKCSEHHISIQKPS-----PAL IPFYKBCGSDGICISDLILDVQQLPAIQTQSF----IVSNQNKRLTFS EVRVCLHVQKSTRDRLREGQIQSVVTYDLALD----SGRPHSRAVFNET : :| | | ::||:| : :|||: )ILMLGAVGAFDWSGTLVQETSHKPVIFPKQAFDQVLQDRNHSSFLGYS VLGAPRYQHIGLVAMFRQNTGMWESNANV----KGTQIGAYFGASLCS DIVITIDIVALGAPGEEDINRGAVYLFHGTSGSGISPSHSQRIAGSKLSPR--ENARGEGOSVVQL---QGSRVVVGAPQEIVAANQRGSLYQC--DYST :: || || || || || || GPSSEQFGXSVQQLTNPQGNWLLVGSPWSGFPENRMGDVXKCPVDLFT QYANEPRIIFNLNDFETKEDMVQATSETRQHGGDLTNTFRAIEFARDY Gaps 18.2%; Score 1071; DB 2; Length 1178; 27.9%; Pred. No. 6.3e-66; ive 208; Mismatches 487; Indels 188; HGVSTKYLNFTASENTSRVMQHQYQVSNLGQR--

| 8 6 8 6 8 8 8   | atelet Cy Cy Cy Cy Cy Cy Cy Cy Cy Cy Cy Cy Cy  |
|---|--|
| Db 929 LLYDAELHLT-RSTNINFYEISSDENAPSVIKSVEDIGPKFIFSLKVTAGSAPVSNA 984  956 FLV | RESULT: Allernate names: CD40). platelet glycoprotein GPIs; VIA-2/collagen receptor alpha-2 c/species: CD40). platelet glycoprotein GPIs; VIA-2/collagen receptor alpha-2 c/species: Homo sapiens: (man) C. Species: Man, Sapiens: (man) C. Species: |

| Qy 617 ARNVFECNDQVVKGKEAGEVRVCLHVQ-KSTRDRLARGQIQSVVTYDLALDSGRPHSR 673  bb 681 NIQKKNCRVEGKETVCINATMCFHVKLKSKEDSIYEADLQYRVTLDSIRQISR 733  Qy 674 AVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCI | 719 NESLOGIELSAFGNILEPLALEDAQRIETALFPEE  717 DENLT-DPENGPVLDDALPNSVHEHIDPRA  717 DENLT-DPENGPVLDDALPNSVHEHIDPRA  717 DENLT-DPENGPVLDDALPNSVHEHIDPRA  718 VGGPRE-FNVTVTVRNDGEDSYRTQVTFFFEDDI  831 VKSQHDKFNVSLTVKNKGDSAXNTRTVVQHSBNI  838 TEVSGALKGTSCSINHPIFPENSEVTFNITFOVN  830 TEVSGALKGTSCSINHPIFPENSEVTFNITFOVN  897 KTEFQLELPVKYAVXMVVTSHGVST  934 DNEVNISIPKYAVCLQFYSSASEHHISVAANET  935 DNEVNISIPKYEVGLQFYSSASEHHISVAANET  946 GQRSLPISLVFLVPVKLNQTY  957 WTFS  | RESULT 12  1ymphocyte-Peyer's patch adhesion molecule alpha 4 precursor - mouse 1ymphocyte-Peyer's patch adhesion molecule alpha 4 precursor - mouse 0;3pecies: Mus musculus (house mouse) 0;3pecies: Mus musculus (house mouse) 0;3pecies: Musculus (house mouse) 0;3pecies: Musculus (house mouse) 0;3pecies: Musculus (house mouse) 0;3pecies: Musculus (house mouse) 0;3pecies: Musculus (house mouse) 0;3pecies: Musculus (house mouse) 0;3pecies: Musculus (house mouse) 1;4pecies: Musculus (house mouse) 1;5pecies: Musculus (house) 1;5pecies: Musculus ( |
|--|--|--|
| Db 1092 VQLTAAABINTYNPEIYVIEDNTVTIPLMIMKPDEKAEVPTGVIIGSIIA 1141 Qy 1101 GLLLLALITAALYKLGFFKRQYKDM 1125   | RESULT 11 A35854 Circgina alpha-1 chain precursor - rat Cispecies: Rattus norvegicus (Norway rat) Cispecies: Rattus norvegicus (Norway rat) Cispecies: Rattus norvegicus (Norway rat) Cispecies: Rattus norvegicus (Norway rat) Cispecies: Rattus norvegicus (Norway rat) Cispecies: Rattus norvegicus (Norway rat) Cispecies: A3-0-1-11 Rignatius, M.J.; Large, T.H.; Houde, M.; Tawil, J.M.; Barton, A.; Esch, F.; Carbonetto, A.; Accession: A35854, MID: 9038125; PMID: 2380249 A.; Accession: A35854 A; Accession: A35854 A; Accession: A35854 A; Accession: A35854 A; Accession: A35854 A; Accession: A35854 A; Accession: A35854 A; Accession: A35854 A; Accession: A35854 A; Accession: A1875 A; Accession: A1875 A; Accession: A1875 A; Accession: A1875 A; Accessi | 166<br>203<br>224<br>227<br>332<br>339<br>339<br>442<br>442<br>454<br>498<br>621   |

| qq | :   :   :  | Db 984 TIIITISL   |
|----|--|---|
| λō | 156 FISTVMEQLKKSKTLFSLMQYSEEFRIHFTFKEFQNNENPRSLIKPITQLLGRTHTATGI 215 | RESULT 13   |
| qa | 186  | S06046<br>integrin alpha-4 chain  |
| λō | 216 RKVVRELFNITNGARKNAFKILILITDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDAF 275 | N; Alternate names: CD49  |
| qq | 196 200  | C;Date: 01-Dec-1989 #se   |
| λö | 276 RSEKSRQELNTVASKPPRDHVFQINNFEALKTIONOLREKIFAIEGTOTGSSSSFEHFMS 335 | R; Takada, Y.; Elices, M  |
| qq |  | A;Title: The primary st.  |
| δý |  | A, Accession: S06046  |
| qa | (1)  | A;Molecule Lype: MKNA A;Residues: 1-1038 <tak a:cross-references:="" ini<="" td=""></tak> |
| ò  |  | Rikosen, G.D., Birkenme   |
| QD | :  :       :  :  <br>EMKGKKLGSYFGASVCA                               | A;Title: Characterization A;Reference mimber: A393  |
| δλ | 448 VDVDSNGSTDLVLIGAPHYYBQTRGGQVSVCPLPRGQRA-RWQCDAVLYGEQGQPWGRFG 506 | A; Accession: A39355<br>A; Molecule type: DNA   |
| qq |  | A;Residues: 1-93 <ros></ros>  |
| δλ | 507 AALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQ 566 | R; Takada, Y.; Strominger<br>Proc. Natl. Acad. Sci. 1                                     |
| qq | 377 ESIANLGDIDNDGFEDIAIGAPQEDDLRGAVYIYNGRV-DGISSTYSQRIEGQQISKSLR 435 | A, Title: The very late a A, Reference number: A94  |
| Qy | 567 YFGQSLSGGQDLTMDGLVVDLTVGAQGHVLLLRSQPVLRVKAIMEFNPREVARNVFECN 624  | A;Accession: D28018<br>A:Molecule type: profest   |
| Ωp |  | A;Residues: 40-50,'E',52<br>C;Genetics:   |
| ζŎ | 625 DQVVKGKEAGEVRVÇLHVQKSTRDRLREGQIQSVVTYDLALDSGRPHSRAVFNET 679      | A;Gene: GDB:ITGA4; CD49I  |
| qq | AESPSRFYFFSNGT   | A; Map position: 2q31-2q3<br>C; Superfamily: integrin                                     |
| Qy | 680 KNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNFSLVGTPLSAFGNLR 734      | C; Keywords: cell adhesic<br>F;1-39/Domain: signal se                                     |
| qa | 548 SDVITGSIRVSSSGEKCRTHQAFMRKDVRDILTPIHVBATYHLGHHVITKRNTEEFPPLQ 607 | F;40-1038/Product: integ  |
| δλ | 735 PVLAEDAQR-LFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVGGPREFNV 787       | Query Match<br>Best Local Similarity  |
| qa | 608 PILQQKKEKDVIRKMINFARFCAYEN-CSADLQVSAKVGFLKPYENKTYLAVGSMKTIML 666 | Matches 249; Conserv  |
| δλ | 788 TVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEVSGALKST 847 | Qy 272 GDAFRSEKSR<br>   |
| ΩP |  | Db 121 GKTCLEERDN   |
| ζ  | TSENNMPRTNKTEFOLELP  | Oy 311 QLREKI   |
| qu |  | Db 181 BLSKRIAPCY   |
| δý |  | Qy 357 DWAGGVFLY-   |
| q  | LTFHVINTGISMAPNVSVKIM  | Db 226 YWIGSLFVYN   |
| δy |  | Qy 412 HIGLVAMFRO   |
| qa | GRECTFAQQKGIAGTLTDIVKFLSKTD  | Db 283 QIGKAYIF   |
| λ  | 1001 KAPVVNCSIAVCORIQCDIPFFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEIL 1058 | Qy 468 EQTRGGQVSV   |
| qa |  | Db 338 TIREEGRVFV   |
| δ  |  | Qy 527 APGEEDNRGA   |
| qq | 934 EMDETSSLKPEIKATAFPEPHPKVIELNKDENVAHVFLEGLHHQRPKRHF 983           | Db 396 APQEDDLQGA   |
| ζ  | VGSSVGGLLLLALITAALYKLGFFKRQYKI                                       | Qy 587 TVGAQGHVI  |
|    |  | Db 455 AVGAFRSDSA   |

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AX>
AIPROT:P13612; GB:X16983; EMBL:X15356; NID:g33945; PIDN:CAA34852.1,
neler, T.M.; Dean, D.C.
V.S.A. 88, 4094-4098, 1991
i.on of the alpha-4 integrin gene promoter.
39355; MUID:91239513; PMID:2034655
                                                                                                                                                                                                                                                                                                     tructure of the alpha(4) subunit of VLA-4: homology to other inter 6046; MUID:89356603; PMID:2788572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   er, J.L.; Hemler, M.E.
N.S.A. 84, 3239-3243, 1987
antigen family of heterodimers is part of a superfamily of molecu
4151; MUID:87204112; PMID:3033341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         n alpha-4 chain
ion; cytoskeleton; duplication; glycoprotein; heterodimer; transme
sequence #status predicted <SIG>
egrin VLA-4 alpha-4 chain #status predicted <MAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----SCQAGISSFYTKDLIVMGAPGSS 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---TSKEKSTFINMTRVDSDMNDAYLGYA--AAIILRNRVQSLVLGAPRYQ 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---SIDEKELNILHEMKGKKLGSYFGASVCAVDLNADGFSDL-LVGAPMQS 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VCPLPRGORARWQC-DAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIG 526
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                                                                                                                                                       very late antigen-4 alpha chain; VLA-4 alpha chain
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LLLGLIVLLLISCVMWKAGFFKRQYKSILQE 1022
                                                                                                                                                                                                                             439355; D28018
M.J.; Crouse, C.; Hemler, M.E.
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                                                                                                                                precursor - human
9d; very late antic
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52-53 <TA2>
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LPSHSDFLAELRKA------PVVNCSIAVCQRIQCDIPFFGIQEEFNATLKGNLSFD 1039
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C;Species: Lytechinus variegatus (variegated urchin)
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QVSNLGQRSLPISLVFL-VPVRLN------QTVIWDRPQVTFSENLSSTCHTKER
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                                                                                                                                                                                                                                                                                                                                                                                                                                          424 RMFGQSISGGIDMDGNGYPDVTVGAFMSDSVVLLRARPVITVD-VSIFLFGSINITAPQC
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EHEMSQEGFSAALTSNGPLLSTVGSYDWAGGVFLYTSKEKSTFINMT-RVDSDMNDAYLG
                                                                                                  YA--AAIILRNRVQSLVLGAPRYQHIGLVAMFR--QNTGMWESNANVKGTQIGAYFGASL
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R;Hertzler, P.L.; McClay, D.R.
submitted to the EMBL Data Library, May 1998
A;Description: Alpha SU2, a sea urchin integrin which binds laminin.
A;Reference number: Z21035
A;Reference number: T31437
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A.Status: perliminary; translated from GB/EMBL/DDBJ
A.Status: neriminary; translated from GB/EMBL/DDBJ
A.Residues: 1-1035 - RES>
A.Cross-references: UNINEOT:Q13797; GB:D25303; NID:G464180; PIDN:BAA04984.1; PID:G533327
A.Cross-references: UNINEOT:Q13797; GB:D25303; NID:G464180; PIDN:BAA04984.1; PID:G533327
Cell Biol. 123, 1289-1297, 1993
A.Title: Sequence and tissue distribution of the integrin alpha9 subunit, a novel partne
A.Aceference number: A49459; MUID:94064789; PMID:8245132
A.Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                             868 FDVDSKASLGNKLLLKANVTSEN--NMPRTNKTEFQLELPVKYAVYMVVTSHGVSTKYLN 925
                                                                                                                                                                                                              754 NCGNDNICQDDLSIT--FSFM----SLDCLVVGGPREFNVTVTVRNDGEDSYRTQVTFFF 807
                                                                                                                                                                                                                                                                                                                                                                                                                                                         LDVSSLSRAEEDLSITVHATCENEEEMDNLKHSRVTVAIPLKYEVKLTVHGFVNPTSFVY
                                                                                                                                                                                                                                                                                                              PLDLSYRKVSTLQNQRSQRSWRLACESASSTEVSGALKSTSCSINHPIFPENSEVTFNIT
                                                                                                                                                                                                                                                                                                                                             686 PVGLYFIKILELEEK-----QINCE---VTDNSGVVQ-LDCSIGYIYVDHLSRIDISFL
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                                                 CESYKGKEVPGYIVLFYNMSLDVNRKAESPPRFYFSSNGTSDVITGSIQVSSREANCRTH
                                                                                                                                                             QAFMRKDVRDILTPİQIEAAYHLGPHVISKRSTEEFPPLQPILQQKKEKDIMKKTINFAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Superfamily: integrin alpha-4 chain c;Keywords: glycoprotein; metal binding; transmembrane protein F;1-27/\text{Domain}: signal sequence #status predicted <SIG>
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                                                                                                                    KLQLPNCIEDPVSPIVLRLNFSLVGTPLS
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A,Residues: 30-1035 <PAL>
A,Cross-references: GB:L24158
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| A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-1041 <her> A;Residues: 1-1041 <her> A;Cross-references: UNIPROT:076378; EMBL:AF067658; NID:g3220240; PID:g3220241; PIDN:AAC2 C;Function: C;Function: A;Description: binds laminin C;Superfamily: integrin alpha-2b chain</her></her> | ; Score 614.5; DB 2; Length 1041;<br>; Pred. No. 3.3e-34;<br>155; Mismatches 314; Indels 245; Gaps 41; | QEGFSAAITSNGPLLSTVGSYDWAGGVFLYTSKEKSTFINMTRVDSDMNDAYLG 389 | YAAAIILRNRVQSLVLGAPRYQHI-GLVAMFRQNTGMWESNANVKGTQIGAYFGASLC 446<br> :  : | SVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPLPRGQRARWQCDAVLYGEQ 498 | GQPWGRFGAALTVLGDVNGDKLTDVALGAPGEEDNRGAVYLFHGTSGS 546 | GISPSHSQRIAGSKLS-PRLQYFGQSLSGGQDLTWDGLVDLTVGAQGHVLLLRSQPVL 603 | RVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSV 658 : | VIYDLALDSG-RPHSRAVFNETKNSTRRQTQVLGL-TQTCETLKLQ 702 | SLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEK 753 | NCGNDNICQDDLSITFSFMSLDCLVVGGPREFNVTVTVRNDGEDSYRTQVTFFFDLDLSY 813 | RKVSTLQNQRSQRSWRLACESASSTEVSGALKSTSCSINHPIFPENSEVTFNIT 867 :: :: | FDVDSKASLGNKL/LLKANVTSENNMPRTNKTEFQLELPVKYAVYNVVTSHGVSTK 922 |                  |                  | NCSIAVCQRIQCDIPFFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILF 1059 | NDSVFTLLPGQGAFVRSQTETKVEPFEVPNPLP 1092 |
|--|--|--|---|--|--|--|---|--|---------------------------------------|--|--|--|------------------|------------------|---|--|
| eliminary; translate<br>Ype: mRNA<br>1-1041 <her><br/>rences: UNIPROT:0763<br/>al source: developme<br/>n: binds laminin<br/>/: integrin alpha-2b</her>  | ch<br>1 Similarity 24.8%;<br>236; Conservative 155   |  | YAAAIILRNRVQSLVL(<br> -  -  -  -  -  -  -  -  -  -  -  -  -             | SVDVDSNGSTDLVLIGAPHYYEQTRGGQV                            | SNRLSLSSTLI  |  |   | CFTYTGNYLPDHI                                      |                                       |  |  | FDVDS<br>    <br>GDKDSIEF                                    |                  |                  |   |  |
| A;Status: pre<br>A;Molecule ty<br>A;Residues: 1<br>A;Cross-refer<br>A;Experimente:<br>A;Punction:<br>A;Description:  | Query Match<br>Best Local<br>Matches 23  | Qy 336<br>Db 181   | Qy 390<br>Db 240  | Qy 447 Db 297  | Qy 499<br>Db 344                                     | Qy 547<br>Db 403   | Oy 604<br>Db 463  | Qy 659<br>Db 498                                   | Qy 703<br>Db 558                      | Qy 754<br>Db 610   | Qy 814<br>Db 668   | Qy 868<br>Db 718   | Qy 923<br>Db 776 | Qy 961<br>Db 835 | Oy 1006<br>Db 893   | Oy 1060                                |

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| 1093 -LIVGSSVGGLLLLALITAALYKLGFFKRQYKDMMSEGGPP 1 |      |  |
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Search completed: November 9, 2004, 12:19:34 Job time: 33.25 secs

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                   Copyright
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- protein search, using sw model OM protein

9 November :00

2004, 11:46:42

; Search time 136.75 Seconds (without alignments) 4783.919 Million cell updates/sec

US-09-902-481B-5

Perfect score:

1 FNLDTENAMTFQENARGFGQ......FKRQYKDMMSEGGPPGAEPQ 1137 Sequence:

**BLOSUM62** 

Scoring table:

1825181 seqs, 575374646 residues Gapop 10.0 , Gapext 0.5 Searched:

1825181 hits satisfying chosen parameters: Total number of

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Listing first 45 summaries Maximum Match 100% Post-processing: Minimum Match 0%

UniProt\_02:\* Database

1: uniprot\_sprot:\* 2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|    | Description    | P11215 homo sapien | mus m      | 09ji30 rattus norv | Q28984 sus scrofa |            | homo       | m snm  | Bad21383 mus muscu | Q9qxh4 mus musculu | Q9qye7 rattus norv | P61625 bos taurus | P20701 homo sapien |        | Aaq90015 bos tauru | P24063 mus musculu | Q9wtv4 mus musculu | Q9r200 mus musculu | Q98tfl cyprinus ca |        |        | Q8hzv0 bos taurus | O88340 rattus norv | Q60677 mus musculu | P38570 homo sapien | O88341 rattus norv | P56199 homo sapien | 5 homo     | bos t      | Q62469 mus musculu | Q6plc7 mus musculu | Aah65139 mus muscu |
|----|----------------|--------------------|------------|--------------------|-------------------|------------|------------|--------|--------------------|--------------------|--------------------|-------------------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|------------|------------|--------------------|--------------------|--------------------|
|    | ID             | ITAM HUMAN         | ITAM MOUSE | 0811 <u>3</u> 0    | Q28984            | ITAX HUMAN | ITAD HUMAN | Q6KAS4 | BAD21383           | ITAX MOUSE         | ITAD RAT           | ITAL BOVIN        | ITAL HUMAN         | Q6TYB8 | AAQ90015           | ITAL MOUSE         | Q9WTV4             | Q9R200             | Q98TF1             | Q96нв1 | Q98TF0 | QBHZV0            | 088340             | ITAE MOUSE         | ITAE HUMAN         | 088341             | ITA1 HUMAN         | ITAH HUMAN | ITA2_BOVIN | ITA2_MOUSE         | Q6P1C7             | AAH65139           |
|    | DB             | <u> </u>           | Н          | ~                  | 7                 | г          | Н          | 7      | 7                  | Н                  | ч                  | Н                 | 1                  | C)     | ~                  | -                  | N                  | 7                  | 7                  | N      | 7      | 7                 | 7                  | 7                  | П                  | 7                  | Н                  | Н          | ч          | 7                  | 7                  | ~                  |
|    | Length         | 1152               | 1153       | 1151               | 920               | 1163       | 1162       | 1188   | 1188               | 1169               | 1161               | 1165              | 1170               | 1166   | 1166               | 1163               | 1161               | 1160               | 1196               | 1086   | 1187   | 927               | 1167               | 1167               | 1179               | 1167               | 1151               | 1189       | 1170       | 1178               | 1178               | 1178               |
| de | Query<br>Match | 99.5               |            | 74.6               |                   | 59.2       |            | 56.7   |                    | 56.5               |                    |                   |                    |        |                    | 26.2               |                    | 25.9               | 24.0               | 23.1   | ë.     |                   | •                  | 19.8               | ٠                  | 19.1               | 18.                | 18.        | 18.        | 18.                | Н                  | 18.2               |
|    | Score          | 5846.5             | 4470       | 4381               | 3809.5            | 3479       | 3411       | 3329.5 | 3329.5             | 3320.5             | 3244.5             | 1583              | 1557.5             | 1557   | 1557               | 1538.5             | 1534.5             | 1524               | 1409               | 1359.5 | 1358.5 | 1278              | 1167.5             | 1161.5             | 1153               | 1123               | 1103.5             | 1093.5     | 1085       | 1011               | 1071               | 1011               |
|    | Result<br>No.  | <br>   <br>        | 7          | æ                  | 4                 | S          | 9          | 7      | 8                  | 6                  | 10                 | 11                | 12                 | 13     | 14                 | 15                 | 16                 | 17                 | 18                 | 13     | 20     | 21                | 22                 |                    |                    |                    | 26                 |            |            |                    |                    |                    |

| P17301 homo sapien | 0/55/8 nomo saplen<br>P18614 rattus norv | 042094 gallus gall | P61622 mus musculu | Q7tqc3 mus musculu | Q8bs01 mus musculu | Q8mkf4 felis silve | Q9wuf8 mus sp. itg | Q8tes5 homo sapien | Q9bpq8 halocynthia | Q63001 rattus norv | Q6pg66 mus musculu | Aah57200 mus muscu |
|--------------------|--|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| ITA2_HUMAN         | ITA1 RAT                                 | 0420 <u>9</u> 4    | ITAH MOUSE         | Q7TQC3             | Q8BS01             | Q8MKF4             | Q9WUF8             | Q8TES5             | Q9BPQ8             | 063001             | Qepge6             | AAH57200           |
| П,                 |  | N                  | Н                  | 7                  | N                  | N                  | N                  | N                  | N                  | 7                  | N                  | 0                  |
| 1181               | 1180                                     | 1171               | 1188               | 1188               | 1038               | 1160               | 895                | 348                | 1332               | 205                | 304                | 304                |
| 18.2               | 18.1                                     | 17.9               | 17.9               | 17.9               | 17.8               | 17.3               | 17.3               | 14.7               | 14.5               | 13.8               | 13.3               | 13.3               |
| 1068               | 1062                                     | 1053               | 1052.5             | 1052.5             | 1045               | 1018.5             | 1018               | 865                | 850                | 808                | 780.5              | 780.5              |
| 32                 | 34                                       | 32                 | 36                 | 37                 | 38                 | 39                 | 40                 | 41                 | 42                 | 43                 | 44                 | 45                 |

## ALIGNMENTS

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SECUENCE FROM N.A.

MEDILIBE-88315033; PubMed=2457584;

MEDILIBE-88315033; PubMed=2457584;

Corbi A.L., Kishimoto T.K., Miller L.J., Springer T.A.;

"The human leukocyte adhesion glycoprotein Mac-1 (complement receptor type 3, CD11b) alpha subunit. Cloning, primary structure, and relation to the integrins, von Willebrand factor and factor B.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLIFES 8130151; MEDLIFES 88.90151; PubMed=2833753; MEDLIFES 88.90151; PubMed=2833753; Arnaout M.A., Remold-O'Donnell E., Pierce M.W., Harris P., Tenen D.G.; Molecular cloning of the alpha subunit of human and guinea pig leukocyte adheaion glycoprotein Mol: chromosomal localization and homology to the alpha subunits of integrins."; Proc. the alpha Sci. U.S.A. 85:2776-2780(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=88257215; PubMed=2454931;
Arnaout M.A., Gupta S.K., Pierce M.W., Tenen D.G.;
Amanou acid sequence of the alpha subunit of human leukocyte adhesion receptor Mol (Complement receptor type 3).";
J. Cell Biol. 106:2153-2158(1988).
                                                     01-JUL-1989 (Rel. 11, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-204 (Rel. 45, Last annotation update)
Integrin alpha-M precursor (Cell surface glycoprotein MAC-1 alpha subunit) (CR-3 alpha chain) (CD11b) (Leukocyte adhesion receptor MO1) (Neutrophil adherence receptor).
Home sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=93123748; PubMed=8419480; MEDLINE=93123748; PubMed=8419480; Pleming J.C., Pahl H.L., Gonzalez D.A., Smith T.F., Tenen D.G.; Structural analysis of the CD11b gene and phylogenetic analysis of the alpha-integrin gene family demonstrate remarkable conservation of genomic organization and suggest early diversification during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Roth G.J.; "CDNA sequence for the alpha M subunit of the human neutrophil adherence receptor indicates homology to integrin alpha subunits.";
                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Hickstein D.D., Hickey M.J., Ozols J., Baker D.M., Back A.L.,
                     PRT; 1152 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 9-1153 FROM N.A.
                   STANDARD;
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            ITAM HUMAN P11215;
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PDB; 1BHO; X-ray; 1/2=-.
PDB; 1BHO; X-ray; 1/2=-.
PDB; 1DN; X-ray; 1/2=-.
PDB; 1IDN; X-ray; 0=140-331.
PDB; 1IDO; X-ray; 0=140-331.
PDB; 1JJM; X-ray; 0=140-331.
PDB; 1MIU; X-ray; 0=144-337.
PDB; 1NPZ; X-ray; A=144-337.
Genew; HGNC: 6149; ITGAM.
MIN; 120980;
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PRINTS; PRO0485; WPFADOWAIN.
SMART; SM00191; Int_alpha; 5:
SMART; SM00327; VWA; 1.
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X_{i}^{\mathcal{M}}
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-!- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins with I-domains do not undergo protease cleavage.
-!- SIMILARITY: Belongs to the integrin alpha chain family.
-!- SIMILARITY: Contains 7 FG-GAP repeats.
-!- SIMILARITY: Contains 1 VWFA domain.
-!- SIMILARITY: WAME-PROW; NOTE-CD guide CD11b entry;
-:- DATABASE: NAME-PROW; NOTE-CD guide CD11b cntry;
-:- WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cdllb.htm".
                                                                                                                                                                                                  MEDLINE=87076671; PubMed=3539202; Pierce M.W., Remold-O'Donnell E., Todd R.F. III, Arnaout M.A.; Pierce M.W., Remold-O'Donnell E., Todd R.F. III, Arnaout M.A.; "N-terminal sequence of human leukocyte glycoprotein Mol: conservation across species and homology to platelet IIb/IIIa."; Biophys. Acta 874:368-371(1986).
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"Two conformations of the integrin A-domain (I-domain): a pathway for
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98362595; PubMed=9687375;
Baldwin E.T., Sarver R.W., Bryant G.L. Jr., Curry K.A.,
Fairbanks M.B., Finzel B.C., Garlick R.L., Heinrikson R.L.,
Horton N.C., Kelley L.L., Mildner A.M., Moon J.B., Mot J.E.,
Mutchler V.T., Tomich C.S., Watenpaugh K.D., Wiley V.H.,
"Cation binding to the integrin CD11b I domain and activation model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Type I membrane protein. TISSUE SPECIFICITY: Predominantly expressed in monocytes and
                     SEQUENCE OF 1-9 FROM N.A.
MEDILINE=92073318; PubMed=1683702;
Shelley C.S., Arnaout M.A.;
"The promocter of the CD11b gene directs myeloid-specific and developmentally regulated expression.";
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Pabll H.L., Rosmarin A.G., Tenen D.G.;
"Characterization of the myeloid-specific CD11b promoter.";
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                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 148-334.
                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 148-337.
                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 148-331.
Proc. Natl. Acad. Sci. U.S.A. 86:257-261(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3D-STRUCTURE MODELING OF 17-616.
MEDLINE=98226734; PubMed=9560195;
                                                                                                                                                                                                                                                                                MEDLINE=95171458; PubMed=7867070;
                                                                                                                                                                                                                                                                                                                                                                                                                   Structure 3:1333-1340(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           associates with beta-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Structure 6:923-935(1998).
                                                                                                       SEQUENCE OF 1-9 FROM N.A.
                                                                                                                                                                                         SEQUENCE OF 17-31.
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| 1 16 17 1152 Integrin alpha-M. 99.5%; Score 5846.5; DB 1; Length 1152; imilarity 99.2%; Pred. No. 0; 1; Conservative 7; Mismatches 1; Indels 1; Gaps FNLDTENAMTPQENARGEGSVVQLQGSRVVVGAPQEIVAANQRGSIYQCDYSTGSCEPIFI | RLQVPVEAVMNSLGLSLAATTSPPQLLACGPTVHOTCSENTYVKGLCFLFGSNLRQOPOK          | EADREGVIRYVIGYGDAFRSEKSRQEINTIASKEPRDHYEQVN AIEGTQTGSSSSFBHEMSQEGFSAAITSNGPLLSTVGSYDWAG AIEGTQTGSSSSFBHEMSQEGFSAAITSNGPLLSTVGSYDWAG AIEGTQTGSSSSFBHEMSQEGFSAAITSNGPLLSTVGSYDWAG RVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR RVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR GAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPL AIHIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII   | PRGORARWQCDAVLYGEQGOPWGRFGAALTVLGDVNGDKLTDVALGAPGEEDNRGAVTLF PRG-RARWQCDAVLYGEQGOPWGRFGAALTVLGDVNGDKLTDVALGAPGEEDNRGAVTLF PRG-RARWQCDAVLYGEQGOPWGRFGAALTVLGDVNGDKLTDVALGAPGEEDNRGAVTLF HGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTVGAQGHVLLIRSQ  | SLUGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLUVG SLUGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLUVG SLUGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLUVG GPREFNUTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEV GPREFNUTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEV SGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRTNKTEF SGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRTNKTEF SGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRTNKTEF SGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRTNKTEF SGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRTNKTEF SGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRTNKTEF SGALKSTSCSINHPIFFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRTNKTEF SGALKSTSCSINHPIFFFFINITFNITFNITFNITFNITFNITFNITFNITFNI   |
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Adachi J., Bono H., Kondo S.,
Uki H., Yamanaka I., Kiyosawa H.,
Jami A., Schonbach C., Gojobori T.,
Hume D.A., Quackenbush J.,
Batalov S., Beisel K.W.,
Dethia C., Corbani L.E., Cousins S.,
T., Forrest A., Frazer K.S.,
C., Godzik A., Gough J.,
Jackson I.J., Jarvis E.D.,
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Lenhard B., Lyons P.A.,
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Leaddale R.D., Tomita M.,
A., Setcou M., Shimada M.,
Wang Y., Matanabe Y., Wells C.,
Guisawa M., Yang I.,
Wang Y., Matanabe Y., Wells
C., Garninci P., Hayatsu M.,
Carninci P., Hayatsu M.,
Carninci P., Hayatsu M.,
Carninci P., Hayatsu M.,
Sakazume M., Sakazume N., Sato K.,
R., Arakawa T., Fukuda S.,
Sahinagawa I.,
Shinagawa A.,
R., Lander E.S., Rogers J.,
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Leukocyte adhesion receptor MO1).
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ional domain related to von
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lathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                eyer W.J., Gee C.E.,
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SIGNAL

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**Springer T.1.** Teplow DB. Dreyer W.J.;

**Springer T.1.**. Teplow DB. Dreyer W.J.;

**Sequence homology of the LFA-1 and Mac-1 leukocyte adhesion

**Sequence homology of the LFA-1 and Mac-1 leukocyte adhesion

**Sequence homology of the LFA-1 and Mac-1 leukocyte interferon.";

**Rature 314:540-542(1985).

**CC -1- FUNCTION: Integrin alpha-M/beta-2 is implicated in various

**CC as well as in mediatring the uptake of complement-coated particles.

**CC It is identical with CR-3, the receptor for the iC3b fragment of

**Liberthogen in CBA: Integrin alpha-M/beta-2 is also a receptor for

**C fibrinogen factor X and ICAMI. It recognizes Pl and P2 peptides

**C fibrinogen gamma chain. Alpha-M/beta-2 play a critical role in

mast cell development and in immune complex-mediated

**Glomerulonephritis. Mice expressing a null mutation of the alpha-M

subunit gene demonstrate increase in neutrophila crumulation, in

response to a impaired degranulation and phagocytosis, events that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibs-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      granulocytes.
-!- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins with I-domains do not undergo protease cleavage.
-!- SIMILARITY: Belongs to the integrin alpha chain family.
-!- SIMILARITY: Contains 7 FG-GAP repeats.
-!- SIMILARITY: Contains 1 VWFA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prem; PRO1839; FG-GAP; 3.
Prem; PRO1839; FG-GAP; 3.
Prem; PRO1835; Integrin_alpha; 1.
Prem; PRO1895; Integrin_alpha; 1.
PRINTS; PRO195; VWA; 1.
PRINTS; PRO1919; Int alpha; 5.
SWART; SMO0191; Int alpha; 5.
SWART; SMO0191; Int alpha; 5.
PROSITE; PSO243; VWFA; 1.
PROSITE; PSO243; VWFA; 1.
PROSITE; PSO243; VWFA; 1.
PROSITE; PSO244; VWFA; 1.
PROSITE; PSO245; VWFA; 1.
Shich profession; Galcium; Cell adhesion; Signal; Transmembrane.
complement receptor type 3 and cellular adhesion molecule Mac-1.";
Proc. Natl. Acad. Sci. U.S.A. 83:5644-5648(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=2;
IsoId=P05555-2; Sequence=VSP 010473;
Note=No experimental confirmation available;
-!- TISSUE SPECIFICITY: Predominantly expressed in monocytes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                obesity.
SUBUNII: Heterodimer of an alpha and a beta chain. Alpha-M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M14293; AAA39484.1; -.
PIR; S00551; S00551.
PIR; S00551; S00551.
MGD; MGI:96607; Itgam.
GO; GO:0009897; C:external side of plasma membrane; IDA.
GO; GO:0007155; P:cell adhesion; IMP.
GO; GO:000453; P:cell adhesion; IMP.
InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; VWF.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      associates with beta-2.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Event=Alternative splicing; Named isoforms=2;
Name=1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId=P05555-1; Sequence=Displayed;
                                                                                         MEDLINE=85188276; PubMed=3887182;
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ilarity 73.9%; Pred. No. 7.9e-287;
Conservative 146; Mismatches 149; Indels
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                   Integrin alpha-M.
Extracellular (Potential).
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Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Fathallah D.M. Sr., Zerria K. Jr.,
Fathallah D.M. Sr., Zerria K. Jr.,
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
-!- SIMILARITY: Belongs to the integrin alpha chain family.
EMBL; AF268593; AAF81280.1; -.
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01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPEALRGCPQEDSDIAFLVDGSGSI1PHDFRRAKEF1STVMEQLKKSKTLFSLMQYSEEF
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                                       IEA
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                                                                                                                                                                                                                                                    126943 MW; 8F785695D4074CA5 CRC64;
                                       pathway;
                                                                                                                                                                                                                                                                                                Best Local Similarity 72.7%; Pred. No. 6.2e-281;
Matches 827; Conservative 150; Mismatches 158;
                                                                                                                                                                                                                                                                                    74.6%; Score 4381; DB 2; 72.7%; Pred. No. 6.2e-281;
GO; GO:0008305; C:integrin complex; IEA.
GO; GO:0007160; P:cell-matrix adhesion; IEA.
GO; GO:0007259; P:integrin-mediated signaling;
InterPro; IPR000413; Integrin_alpha.
Pfam; PF01885; VWF.A.
Pfam; PF01885; FG-GAP; 2.
Pfam; PF00095; VWA; 1.
                                                                                                                               PRINTS; PRO118; INTEGRINA.
PRINTS; PR0148; INTEGRINA.
PRINTS; PR0045; INT_alpha; S.
SMART; SM00191; Int_alpha; S.
SMART; SM00327; VWA; 1.
PR0SITE; PS00242; INTEGRIN_ALPHA; 1.
PR0SITE; PS50234; VWRA; 1.
Cell adhesion; Integrin; Transmembrane.
SEQUENCE 1151 AA; 126943 WW; 8F785695
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VPVRLNQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQC 1017
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                                                                           QINNFEALKTIQNQLREKIFAIEGTQTGSSSSFEHEMSQEGFSAAITSNGPLLSTVGSYD
                                                                                                                                                                                       ILITDGEKFGDPLGYEDVI PEADREGVIRYVIGVGDAFRSEKSRQELNTVASKPPRDHVF
                       WAGGVELYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVA
                                                                                                                                                                                                                                           MFRQNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSV
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P20702; QBRVA6;
01-FEB-1931 (Rel. 17, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Integrin alpha-X precursor (Leukocyte adhesion glycoprotein p150,95
alpha chain) (Leukocyte adhesion receptor p150,95)
Name=ITGAX; Synonyme=CD11C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata, Vertebrata, Buteleostomi,
Catarrhini, Hominidae, Homo.
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Mammalia; Butheria; Primates;
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SEQUENCE FROM N.A.
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                                                                                                                                                                  QLELPVXXAVYMVVTSHGVSTKYLNFTASENTSRVMQHQYQVSNLGQRSLPISLVFLVPV 960
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                                                                                                                                                                                                                                                                                                                                                                                                                                  The SEQUENCE FROM N.A.

ESCUENCE FROM N.A.

LE SEQUENCE FROM N.A.

LE LIE J.-K., Schook L.B., Rutherford M.S.;

LE SIDELLITE Schook L.B., Rutherford M.S.;

LE SUBCELLUTAR LOCATION: Type I membrane protein (By similarity).

-1. SINDLARITY: Belongs to the integrin alpha chain family.

REMBL; U40072; ARB16869.1;

REMBL; U4007160; PRO11 complex; IEA.

RO; GO:0007160; PRO11 matrix adhesion; IEA.

RITHERPO; IPR000413; Integrin_alpha.

RITHERPO; IPR000413; Integrin_alpha.

REMBL; PR01185; RUTERINA.

REMINTS; PR01185; INTERRINA.

REMINTS; PR01185; INTERRINA.

REMART; SM00191; Int alpha; 4.
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                                                                                                             GPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEV
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Sus.
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Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae,
NCBI_TaxID=9823,
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Last sequence update)
Last annotation update)
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Cell adhesion; Integrin; Transmembrane.
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01-FEB-1997 (TrEMBLrel. 05
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CD11b (Fragment).
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SEQUENCE OF 20-43.

SEQUENCE OF 20-43.

MIDLINE-87167596; PubMed=3549901;

MILLER L.J., Wiebe M., Springer T.A.;

"Purification and alpha subunit N-terminal sequences of human Mac-1 and pla0; 95 leukcoyte adhesion proteins.";

J. Immunol. 138:2381-2383 (1987).

-!- FUNCTION: Integrin alpha-X/beta-2 is a receptor for fibrinogen. It recognizes the sequence G-P-R in fibrinogen. It mediates cell-cell interaction during inflammatory responses. It is especially important in monocyte adhesion and chemotaxis.

-!- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-X Corbi A.L., Miller L.J., O'Connor K., Larson R.S., Springer T.A., "CDNA cloning and complete primary structure of the alpha subunit of a leukocyte adhesion glycoprotein, p150,95."; EMBO J. 6:4023-4028(1987). granulocytes.

DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins with I-domains do not undergo protease cleavage.

SIMILARITY: Contains to the integrin alpha chain family.

SIMILARITY: Contains 7 FG-6AP repeats.

SIMILARITY: Contains 1 VWFA domain.

DATABASE: NAME-PROW; NOTE-CD guide CD11c entry;

WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd11c.htm". Corbi A.L., García-Aguilar J., Springer T.A.;
"Genomic structure of an integrin alpha subunit, the leukocyte p150,95
molecule."; associates with beta-2. SUBCELLULAR LOCATION: Type I membrane protein. TISSUB SPECIFICITY: Predominantly expressed in monocytes and Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). Corbi A.L., Garcia-Aguilar J., Springer T.A.; J. Biol. Chem. 265:12750-12751(1990). Biol. Chem. 265:2782-2788(1990), MEDLINE=88166645; PubMed=3327687; SEQUENCE FROM N.A. MEDLINE=90153906; PubMed=2303426;

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N-linked (GlcNAc. . .) (Pote
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N-linked (GlCNAc...)
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T -> S (in Ref. 4).
T -> A (in Ref. 4).
T -> S (in Ref. 4).
G -> A (in Ref. 2).
G -> A (in Ref. 2).
E -> K (in Ref. 2).
I -> V (in Ref. 1).
I -> V (in Ref. 1).
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FG-GAP 2.
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FG-GAP 4.
FG-GAP 5.
FG-GAP 6.
FG-GAP 7.
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M29482; AAAS1620.1; JOINED.
M29483; AAAS1620.1; JOINED.
M29484; AAAS1620.1; JOINED.
M29485; AAAS1620.1; JOINED.
M29486; AAAS1620.1; JOINED.
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PDB; 1N3Y; X-ray; A=141-338.
Genew; HGNC:6152; ITGAX.
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EMBL; M81695; AAA59180.1; -.

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                                                                                                                                                                                                                                                                                                PVLRVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVT
                                                                SLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVG
                                                                                                              GPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTBV
                                                                                                                                                               QLELPVKYAVYMVVTSHGVSTKYLNFTAS-ENTSRVMQHQYQVSNLGQRSLPISLVFLVP
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                                                   YDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=56111956; PubMed=8777714; Van der Veren M., Le Trong H., Wood C.L., Moore P.F., St John T., Van der Vieren M., Le Trong H., Wood S.L., Moore P.F., St John T., Staunton D.E., Gallatin W.M.; "A novel leukointegrin, alpha d beta 2, binds preferentially to ICAM-
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16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Integrin alpha-D precursor (Leukointegrin alpha
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"Structural and functional characterization of
gene CDILd. Essential role of Spl and Sp3.";
J. Biol. Chem. 275:8959-8969(2000)
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Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
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TISSUE=Spleen;
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                                                                                                                                                                                                                                                                                                                        127886 MW; 83658A13B5C5DE8F CRC64;
                                                                                                                                                                                                                                                                                                                                            Score 3479; DB 1;
Pred. No. 3.6e-221;
1; Mismatches 292;
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2. Exp. Med. 188:2187-2191(1998).

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1). In Internative ingulation for vascular cell adhesion molecule 1 (VCAM-1).";

1). In Internation with VCAM1.

M. Crowe D.T. Hoekstra D., Vazeux R., Hoffman P.A., A van der Viaeran M., Crowe D.T., Hoekstra D., Vazeux R., Hoffman P.A., A range interface between 1 domain and VCAM-1: evidence for a binding interface between 1 domain and VCAM-1: evidence for a J. Immunol. 163:1984-1990(1999).

J. Immunol. 163:1984-1990(1999).

C.-- FUNCTION: Integrin alpha-D/beta-2 is a receptor for ICAM3 and VCAM1. May play a role in the atherosclerotic process such as clearing lipoproteins from plaques and in phagocytosis of bloodborne pathogens, particulate matter, and senescent erythrocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TISSUE SPECIFICITY: Expressed moderately on myelomonocytic cell
lines and subsets of peripheral blood leukocytes and strongly on
tissue-specialized cells, including macrophages foam cells within
atherosclerotic plaques, and on splenic red pulp macrophages.
-!- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins
with I-domains do not undergo protease cleavage.
-!- SIMILARITY: Belongs to the integrin alpha chain family.
-!- SIMILARITY: Contains I VWFA domain.
                         MEDLINE=99059842; PubMed=9841932; Grayson M.H., Van der Vieren M., Sterbinsky S.A., Michael Gallatin W., Hoffman P.A., Staunton D.E., Bochner B.S.; "alphadbeta2 integrin is expressed on human eosinophils and functions
                                                                                                                                         as an alternative ligand for vascular cell adhesion molecule 1 (VCAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO1185; INTEGRINA.
PRINTS; PRO0453; VWFADOMAIN.
SMART; SM00191; Int alpha; 5.
SMART; SM00327; VWA; 1.
PROSITE; PS00242; INTEGRIN ALPHA; 1.
PROSITE; PS50234; VWFA; 1.
Calcium, Cell adhesion; Glycoprotein; Integrin; Magnesium; Receptor; Signal; Transmembrane.
I 17 Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-D associates with beta-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIM; 602453; -. GO; 6008305; C:integrin complex; TAS. GO; GO:0008305; C:integrin complex; TAS. GO; GO:00016337; P:cell-cell adhesion; NAS. GO; GO:0005955; P:immune response; NAS. InterPro; IPR00413; Integrin_alpha. InterPro; IPR002035; VWF.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U37028; AAB38547.1; EMBL; U40274; AAB60634.1; EMBL; U40275; AAB60635.1; EMBL; U402776; AAB60636.1; EMBL; U40277; AAB60637.1; EMBL; U40279; AAB60637.1; EMBL; U40279; AAB60638.1; EMBL; U40279; AAB60638.1; U40278; AAB60638.1; U40278; P112.15.1189.1
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Pfam; PF00357; Integrin_alpha; 1.
Pfam; PF00092; VWA; 1.
INTERACTION WITH VCAM1
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61 RLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLRQQPQK 120
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Potential.
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By similarity.
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                                                                                                                                                                                                           19;
                                                                                                                                                                                  Length 1188;
                                                                                                                                                                                 Query Match 56.7%; Score 3329.5; DB 2; Length Best Local Similarity 56.9%; Pred. No. 3e-211; Matches 649; Conservative 170; Mismatches 302; Indels
                                                                                                                                                        CRC64;
                                                                                                                                                        131248 MW; B8D93107BDBB4178
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                                             PRINTS, PROU185; INTEGRINA.
PRINTS; PRO1185; INTEGRINA.
SMART; SMO0191; Int. alpha; 5.
SMART; SMO0191; Int. alpha; 5.
PROSITE; PSO0242; INTEGRIN ALPHA; UNKNOWN_1.
PROSITE; PSS0234; VWPA; 1.
Cell adhesion; Integrin; Transmembrane.
NON_TER
InterPro; IPR002035; VWF_A.
Pfam; PF01089; FG-GAP; 3.
Pfam; PF00057; Integrin_alpha;
Pfam; PF00092; VWA; 1.
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                                                                               HGASESGISPSHSQRIASSQLSPRLQYFGQALSGGQDLTQDGLMDLAVGARGQVLLLRSL
                                                                                                                    PVLRVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVT
                                                                                                                                   YDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNF
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                                                                 HGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTVGAQGHVLLLRSQ
                                                                                                                                                                                                                                                                                                                               SGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRTNKTEF
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               PRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLF
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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05-JUL_2004 (TrEMBLrel. 27, Last sequence update)
05-JUL_2004 (TrEMBLrel. 27, Last annotation update)
MFLJ00114 protein (Fragment).
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GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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05-JUL-2004 (Rel. 44, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
105-JUL-2004 (Rel. 44, Last annotation update)
11tegrin alpha-X precursor (Leukocyte adhesion calpha chain) (Leukocyte adhesion receptor pls0,
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                                             SLPISLVFLVPVRLNQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNCS
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                   LACESASSTEVSGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Okazaki N., Kikuno R., Ohara R., Inamoto S., Koeeki H., Hiraoka S., Saga Y., Kitamura H., Nakagawa T., Nagase T., Ohara O., Koga H.; "Prediction of the Coding Sequences of Mouse Homologues of FLJ Gene: The Complete Nucleotide Sequences of 110 Mouse FLJ-homologous cDNAs Identified by Screening of Terminal sequences of cDNA Clones Randomly Sampled from Size-Fractionated Libraries."; Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                              "Isolation of genes selectively expressed by dendritic cells.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.

"Isolation of genes part of the EMBL/GenBank/DDBJ databases.

"Isolation Integrin alpha-X/beta-1 is a receptor for fibrinogen. It recognizes the sequence G-P-R in fibrinogen. It mediates cell-cell interaction during inflammatory responses. It is especially interaction during inflammatory responses. It is especially interaction monocyte adhesion and chemotaxis (By similarity).

"Isolation and alpha and a beta subunit. Alpha-X associates with beta-2 (By similarity).

"Isolation and alpha and a beta subunit. Alpha-X associates with beta-2 (By similarity).

"Isolation and alpha and a beta subunit. Alpha-X associates with beta-2 (By similarity).

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"Isolation and alpha-X associates are contains 1 VWFA domain.
                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as as long as its content is in no way mondified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PROSITE; PS50234; VWPA; 1.
Calcium; Cell adhesion; Glycoprotein; Integrin; Magnesium; Receptor;
Gorski K., Tong C., Rattis F.-M., Tseng S.-Y., Pardoll
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Extracellular (Potential)
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FG-GAP 3.

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FG-GAP 7.

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GO; GO:0009997; C:sexternal side of pl:
InterPro; IPR000413; Integrin_alpha.
InterPro; IRR002035; WWF-A.
Pfam; PF01899; FG-GAP; 3.
Pfam; PF00189; IRG-GAP; 3.
Pfam; PF00057; Integrin_alpha; 1.
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SIGNAL 1 19
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PRINTS; PR00483; VWFADOMAIN.
SMART; SM00191; Int_alpha; 5.
SMART; SM00327; VWA; 1.
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                                                     Length 1169;
                                                                                                       19;
129150 MW; C616412033C219A6 CRC64;
                                               56.5%; Score 3320.5; DB 1; 56.8%; Pred. No. 1.1e-210; ive 172; Mismatches 302;
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CARBOHYD
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                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                 IAVCORIQCDIPFFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLP
                                      1069 GOGAFVRSQTETKVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMMSE
                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00242; INTEGRIN_ALPHA; 1.
PROSITE; PS50234; VWFA; 1.
Calcium; Cell adhesion; Glycoprotein; Integrin; Magnesium; Receptor;
                                                                                                                                                                                                             STRAIN=Sprague-Dawley;
O'Brien M.M., VanderVieren M., Kilgannon P.D., Dietsch G.
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Extracellular (Potential)
Potential.
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                                                                                                                            (Rel. 44, Last sequence update) (Rel. 44, Last annotation update)
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InterPro; IPR02035; VWF_A.
Pfam, PF01089; RG-GAP, 3.
Pfam, PF00092; VWA, 1.
Pfam, PF00092; VWA, 1.
PRINTS; PR00185; INTEGRINA.
PRINTS; PR00191; Int_alpha; 5.
SWART; SW00191; Int_alpha; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF021334; AAF21241.1; -.
HSSP; P11215; 1BHQ.
                                                                                                         Q9QYE7;
05-JUL-2004 (Rel. 44, Created)
05-JUL-2004 (Rel. 44, Last seq
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SIGNAL 1 19
CHAIN 20 1161
                                                                                                                                           Integrin alpha-D precursor.
                                                                                                  STANDARD;
                                                                                                                                                            Rattus norvegicus (Rat)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              320 FAALRSIQRQLQEKIFAIEGTQSRSSSFQHEMSQEGFSSALTSDGPVLGAVGSFSWSGG 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEALKTIQNQLREKIFAIEGTQTGSSSSFEHEMSQEGFSAAITSNGPLLSTVGSYDWAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       380 AFLYPPNTRPTFINMSQENVDMRDSYLGYSTAVAFWKGVHSLILGAPRHQHTGXVVIFTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            440 EARHWRPKSEVRGTQIGSYFGASLCSVDVDRDGSTDLVLIGAPHYYEQTRGGQVSVFPVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          500 -GVRGRWQCEATLHGEQGHPWGRFGVALTVLGDVNGDNLADVAIGAPGEESRGAVYIFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSTGSCEPIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13; Gaps
                                                                                                                                                                                                                                                                                                      (Potential).
(Potential).
(Potential).
(Potential).
(Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tch 55.2%; Score 3244.5; DB 1; Length 1161; al Similarity 57.6%; Pred. No. 1.2e-205; 649; Conservative 163; Mismatches 302; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                         (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                    (Potential)
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N-linked (GlONAC.)
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Potential.
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FG-GAP
FG-GAP
FG-GAP
             VWFA.
FG-GAP
FG-GAP
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1161 AA; 126600 MW;
             Query Match
Best Local Similarity
Matches 649; Conserv
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Contains 7 FG-GAP repeats.
Contains 1 VWFA domain.
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Potential.
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FG-GAP 2.
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FG-GAP 4.
FG-GAP 5.
FG-GAP 6.
FG-GAP 7.
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N-linked
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                                                                                                                     EMBL; AY267467; AAP94035.1;
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            SIMILARITY:
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                                                                                                                                                                                                                                                                                                                               LELPVKYAVYMVVTSHGVSTKYLNFTASENTSR-VMQHQYQVSNLGQRSLPISLVFLVPV 960
                                                                                                                                                                                                                                           721
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                                                                                                                                          PREFINVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEVS 841
                                                                                                                                                       SPELIVIVIVWNEGEDSYGTLVKFYYPAGLSYRRVIGTQ-QPHQYPIRLACEAEPAAQED 854
                                                                                                                                                                                     901
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SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins with I-domains do not undergo protease cleavage.

SIMILARITY: Belongs to the integrin alpha chain family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
1ntegrin alpha-L precursor (Leukocyte adhesion glycoprotein LFA-1
alpha chain, (LFA-1A) (Leukocyte function associated molecule 1, alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T-cell
                                                                                                                                                                                                        --LRSSSCSINHPIFREGAKTTFMITFDVSYKAFLGDRLLLRAKASSENNKPDTNKTAFQ
                                                                   LVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVGG
                                                                                                              GALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRINKTEFQ
             VLRVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVTY
                                LLKVELSIRFAPMEVAKAVYQCWERTPTVLEAGEATVCLTVHKGSPDLL--GNVQGSVRY
                                                       DLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNFS
                                                                                                                                                                                                                                                                         RLNQTVIWDRPQVTFSENLSS-TCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    glycoproteins.",

Gene 325:97-101(2004).

-- FWOCTION: Integran alpha-L/beta-2 is a receptor for ICAM1, ICAM2,

-- FWOCTION: Integran alpha-L/beta-2 is a receptor for ICAM1, ICAM2,

ICAM3 and ICAM4. It is involved in a variety of immune phenomena
including leukocyte-endothelial cell interaction, cytotoxic T-cel
mediated killing, and antibody dependent killing by granulocytes
and monocytes (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

PubMed=14697514; DOI=10.1016/j.gene.2003.09.043;

Fett T., Zecchinon L., Baise E., Desmecht D.;

"The bovine (Bos taurus) CD11a-encoding cDNA: molecular cloning,
                                                                                                                                                                                                                                                                                                                                                           TKVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMM 1126
                                                                                                                                                                                                                                                                                                                                                                         characterisation and comparison with the human and murine
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1165 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                            P01625;
05-JUL-2004 (Rel. 44, Last seq
05-JUL-2004 (Rel. 44, Last seq
05-JUL-2004 (Rel. 44, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9913;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chain) (CD1
Name=ITGAL;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation—the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OKFPEALRGCPOEDSDIAFLVDGSGSIIPHDFRRAKEFISTVMEQLKKSKTLFSLMQYSE
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                                                                                                                                                                                                                                                      PROSITE; PS00242; INTEGRIN ALPHA; 1.
PROSITE; PS50234; VWFA; 1.
Calcium; Cell adhesion; Glycoprotein; Integrin; Magnesium; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26.9%; Score 1583; DB 1; Length 1165; 35.1%; Pred. No. 1.4e-95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128725 MW; DAEB3A3F1E1463CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                  Integrin alpha-L.
Extracellular (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytoplasmic (Potential) FG-GAP 1.
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GFFKR motif.
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chain) (LFA-1A) (Leukocyte function associated molecule 1, alpha

Euteleostomi;

Catarrhini, Hominidae; Homo

Craniata; Vertebrata;

Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; Name=ITGAL; Synonyms=CD11A;

NCBI\_TaxID=9606;

Homo sapiens (Human)

(CD11a).

Larson R.S., Corbi A.L., Berman L., Springer T., "Primary structure of the leukocyte function-associated molecule-1 alpha subunit: an integrin with an embedded domain defining a protein

Cell Biol. 108:703-712(1989). [2] SEQUENCE FROM N.A. (ISOFORM 2)

superfamily.";

SEQUENCE FROM N.A. (ISOFORM 1), AND PARTIAL SEQUENCE. MEDITHE=81139587; PubMed=2537322; Larson R.S., Corbi A.L., Berman L., Springer T., "Primary structure of the leukocyte function-associat

FROM N.A.

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1048 HLLIVSTAEILFNDSVFTLLPGQGAFVRSQTETKVEPFEVPNPLPLIVGSSVGGLLLLAL 1107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  988 RLPSHSDFLAELRKAPVVNCSIAVCQRIQCDIPFFGIQEEFNATLKGNLSFDWYIKTSHN 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----SCSFGT--EFRCPIDF---RQEILVQVNGMVELRGTIKAS-S 1043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1044 MLSLCSSLAISFNSSKHFHLYGRNASM-AQVVMKVDLVYEKEMLYLYVLSGIGGLLLLFL 1102
                   AGGFLDLKADLKSSTFVGNEPLTVESRAGYLGYTVTWLPSRGTMSLLATGAPRYQHVGRV 430
                                                                                                                                                                                                                         711
LITDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQEINTVASKPPRDHVFQ 298
                                                                                                LDTFEKLKDLFTELOKKIYVIEGTSKODLTSFNMELSSSGISADLSEGHGVVGAVGAKDW 370
                                                                                                                                                                                                   AMFRQ---NIGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQ 474
                                                                                                                                                                                                                                                                     VSVCPLPRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNR 534
                                                                                                                                                                                                                                                                                                                                                                                                             651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPINVSLSYSLWEEEGTPRDPRALDRDIPPILKPSPHLETKEIPFEKNCGEDKNCEADLK 779
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                                                                 INNFEALKTIQNQLREKIFAIEGTQTGSSSSFEHEMSQEGFSAAITSNGPLLSTVGSYDW
                                                                                                                                  AGGVF-LYTSKEKSTFINMTRVDSDMNDAYLGYAAA-IILRNRVQSLVLGAPRYQHIGLV
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ANGSTROMS) OF 153-335, AND REVISION

X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMEDLINE=96036067; PubMed=7479767;

Qu A., Leahy D.J.;
"Crystal structure of the I-domain from the CD11a/CD18 (LFA-1, alpha
beta 2) integrin.";

Proc. Natl. Acad. Sci. U.S.A. 92:10277-10281(1995)

ANGSTROMS) OF 153-335

MEDLINE=96398682; PubMed=8805579;

X-RAY CRYSTALLOGRAPHY (2.0

MEDLINE=99425270; PubMed=10493829; Kalush F., Brandon R., Chftus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon R., Fubrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L., Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S., Eichler E.B., Harris P.C., Venter J.C., Adams M.D.; Genome duplications and other features in 12 Mb of DNA sequence human chromoscae 16p and 16q."; Genomics 60:295-308(1999).

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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J. MOL. Biol. 292:1-9(1999).
J. FUNCTION: Integrin alpha-L/beta-2 is a receptor for ICAM1, ICAM2,
ICAM3 and ICAM4. It is involved in a variety of immune phenomena
including leukocyte-endothelial cell interaction, cytotoxic I-cell
mediated killing, and antibody dependent killing by granulocytes
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MEDLINE=99425288; PubMed=10493852;
Kallen J., Welzenbach K., Ramage P., Geyl D., Kriwacki R., Legge G.,
Cottens S., Weltz-Schmidt G., Hommel U.;
"Structural basis for LFA-1 inhibition upon lovastatin binding to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- DOMAIN: The integrin I-domain (insert) is a vWFA domain.
with I-domains do not undergo protease cleavage.
-!- SIMILARITY: Belongs to the integrin alpha chain family.
-!- SIMILARITY: Contains 7 FG-GAP repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cdlla.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Qu A., Leahy D.J.;
"The role of the divalent cation in the structure of the CD11a/(CD18 integrin.";
Structure 4:931-942(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DATABASE: NAME=PROW; NOTE=CD guide CD11a entry;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note=No experimental confirmation available, TISSUB SPECIFICITY: Leukocytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=2;
IsoId=P20701-2; Sequence=VSP_002738;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           associates with beta-2.
-!- SUBCELLULAR LOCATION: Type I membrane
-!- ALTERNATIVE PRODUCTS:
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141 LQGRPGFQECIKG----NVDLVFLFDGSMSLQPDEFQKILDFWKDVMKKLSNTSYQFAAV 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            310 FVKILDTFEKLKDLFTELQKKIYVIEGTSKQDLTSFNMELSSSGISADLSRGHAVVGAVG 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIRLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLR--- 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QYSEEFRIHFTFKEFQNNPNPRSLIKPITQLLGRTHTATGIRKVVRELFNITNGARKNAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FNLDTENAMTFQ - - ENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSTGSCE
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  Q -> QGVHGLVEMQTSKQILCRPAGDAEHTVG
PWGVSEARRDNIRAGPCR (in isoform 2)
FTId=VSP_002738.
R -> W (in Ref. 1 and 2).
Y -> I (in Ref. 2).
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                                                                                                                                                           R EMBL; AC00230; CAA088'4'.1; -.

R EMBL; AC00230; CAA088'4'.1; -.

R PIB; S03308; S03308

R PIB; ILGP; X-ray; A/B=153-334.

R PDB; ILGQ; NNR; A=149-36.

R PDB; ILGQ; NNR; A=159-336.

R PDB; ILMO; X-ray; A/B=-15-331.

R PDB; ILMO; X-ray; A/B=-15-330.

R PDB; ILMO; X-ray; A/B=150-336.

R PDB; ILMO; X-ray; A/B=150-336.

R PDB; ILMO; X-ray; A/B=150-336.

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R PDB; ILMO; X-ray; A/B=150-336.

R PDB; ILMO; X-ray; A/B=150-336.

R PDB; ILMO; X-ray; A/B=150-336.

R PDB; ILMO; X-ray; A/B=150-336.

R PDB; ILMO; X-ray; A/B=150-336.

R PDB; ILMO; X-ray; A/B=150-336.

R GO; GO:0008305; C:integrin complex; TAS.

R GO; GO:0008305; C:integrin alpha.

R InterPro; IPRO00413; Integrin alpha.

R InterPro; IPRO00413; Integrin alpha.

R PFam; PRO0082; VWRA, 1.

R PRINTS; PRO0148; INTEGRINA.

R PRINTS; PRO0453; VWRADOMAIN.

R SMART; SMO0191; Int alpha; 5.

R RART; SMO0191; Int alpha; 1.

R PRINTS; PRO0444; VWRA, 1.

R PROSITE; PS00242; INTEGRINA ALPHA; 1.

R PROSITE; PS00242; INTEGRINA ALPHA; 1.

R PROSITE; PS00242; INTEGRINA ALPHA; 1.

R PROSITE; PS00242; INTEGRINA ALPHA; 1.

R PROSITE; PS00242; INTEGRINA ALPHA; 1.

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R PROSITE; PS00242; INTEGRINA ALPHA; 1.
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FG-GAP 6.
FG-GAP 6.
FG-GAP 6.
FG-GAP 6.
FG-GAP 6.
FG-GAP 7.
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                                        GEEDNRGAVYLFHGTSGSGISPSHSORIAGSKLSPRLOYFGOSLSGGODLTMDGLVDLTV 588
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  RGGRVFIY-----QRRQLGFEEVSELQGDPGYPLGRFGEAITALTDINGDGLVDVAVGAP 544
                                                                                                                                            QDLISPINVSLNFSLWEEEGTPRDQRAQGKDIPPILRPSLHSETWEI-----PFEKNCGE
                                                                    DRLREGQI QSVVTYDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCI
                                                                                                                                                                                                                               834 ML----KPHSQIPVSCEELPEESRLLSRAL---SCNVSSPIFKAGHSVALQMMFNTLVNSS
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                                                                                                                       GAQGHVLLLRSQPVLRVKAIMEFNPREVARNVFECNDQVV-KGKEAGEVRVCLHVQKSTR
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Dileepan T., Thumbikat P., Kannan M.S., Maheswaran S.K.;

Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.

-!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

EMBL; ANY32558; AAQ90015.1;

InterPro; IPR000413; Integrin_alpha.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lymphocyte function-associated antigen 1 alpha subunit CD11a
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Last annotation update)
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Pfam, PF000357; Integrin_alpha; 1.
Pfam, PF00092; VWA; 1.
PRINTS; PR01185; INTEGRINA.
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NCBI_TaxID=9913;
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                                                                                                                                                                                                                                                                                                                                          PUTLS -- SNYTSKYLGMTLATDPTSDNLLACDPGLSRTCDQNIYLSGLCYLIHENLRGPV
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                                                                                                                                                                                                                                                    25 YNLDVRHVQNFSFPLAGRHFGYRVLQV-GNGVVVGAPSE----GNSMGNLYQCQPETGDCL
                                                                                                                                                                                                                                                                                                          PIRLOVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLRQQP
                                                                                                                                                                                                                                                                                                                                                                                  119 QKFPEALRGCPQEDSDIAFLVDGSGSIIPHDFRRAKEFISTVMEQLKKSKTLFSLMQYSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LITDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTVASKPPRDHVFQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||| : |||:|||:|| 372 AGGFLDLKADLKASTFVGNEPLTVESRAGYLGYTVTRLPSRGTMGLLATGAPKYQHVGRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AMFRO--NTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HVPVGCEELPEEAVVHS-RALSCNVSSPIFGEDSMVDIQVMFNTLQKGSWGDF1ELQANV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EFRIHFTFKEFQNNPNPRSLIKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           595 LLLRSQPVLRVKAIMEFNPREVARNVFECNDQVVKGKEAG-EVRVCLHVQK--STRDRLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWRLACESASSTEVSGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANV
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                                                                                                                                                                                            106;
                                                                                                                                                    Length 1166;
                                                                                                                                                                                            Indels
                                                                                            Transmembrane.
723 MW; 7B8D8AFBA896C9DF
                                                                                                                                                  Query Match 26.5%; Score 1557; DB 2;
Best Local Similarity 34.6%; Pred. No. 7.6e-94;
Matches 409; Conservative 198; Mismatches 469;
                                                  PROSITE, PS00242; INTEGRIN ALPHA; 1.
PROSITE, PS50234; VWFA; 1.
Cell adhesion; Integrin; Transmembra
                                                                                            Integrin; Transm
6 AA; 128723 MW;
PRINTS; PR00453; VWFADOMAIN.
SMART; SM00191; Int_alpha; 5
SMART; SM00327; VWA; 1.
                                                                                                            1166 AA;
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EGQIQSVVTYDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPV 711
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01-MAR-1992 (Rel. 21, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Integrin alpha-L precursor (Leukocyte adhesion glycoprotein LFA-1
alpha chain) (LFA-1A) (Leukocyte function associated molecule 1, alpha
                                                                                                                                                                                                                                                                                                                                      AMFRQ--NTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQ
                  VSVCPLPRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNR
                                                                              VFIY---QXIQLEFQMVSELQGETGYPLGRFGAAIAALTDINGDELTDVAVGAPLEE--O
                                                                                                                            GAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTVGAQGHV
                                                                                                                                                LLLRSQPVLRVKAIMEFNPREVARNVFECNDQVVKGKEAG-EVRVCLHVQK--STRDRLR
                                                                                                                                                                                                              SPIVLRINFSL---VGTPLS--AFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLS
                                                                                                                                                                                                                                                                                                                                                                                   767 ITFSFMSLDCLVVGGPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQR
                                                                                                                                                                                                                                                                                                                                                                                                          SWRLACESASSTEVSGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              838 HVPVGCEELPEEAVVHS-RALSCNVSSPIFGEDSMVDIQVMFNTLQKGSWGDFIELQANV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TS------ENNMPRTNKTEFQLELPVKYAVYMVVTSHGVSTKYLNFTASENTSRVMQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            897 SCNNEDSSLLEDNSATTS-----IPVMYPINVLTKDQENSTLYISFTPKSPRIHHVKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QYQV----SNLGQRSLPISLVPLVPVRLNQTVI---WD---RPQVTFS-ENLSSTCHTKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 988 RLPSHSDFLAELRKAPVVNCSIAVCQRIQCDIPFFGIQEEFNATLKGNLSFDWYIKTSHN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-12468576; PubMed=2051027;
Kaufmann Y., Tseng E., Springer T.A.;
"Cloning of the murine lymphocyte function-associated molecule-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata, Vertebrata, Euteleostomi
Sciurognathi, Muridae, Murinae, Mu
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Eukaryota, Metazoa, Chordata,
Mammalia, Butheria, Rodentia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chain) (CD11a).
Name=Itgal; Synonyms=Lfa-1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
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                                                                                                                                             -----SCSFGT--EFRCPIDF---RQEILVQVNGMVELRGTIKAS-S 1044
                                                                                                                                                                             1048 HILIVSTAEILFNDSVFTLLPGQGAFVRSQTETKVEPFEVPNPLPLIVGSSVGGLLLLAL 1107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25 YNLDVRHVQNFSFPLAGRHFGYRVLQV-GNGVVVGAPSE---GNSMGNLYQCQPETGDCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 PVTLS--SNYTSKYLGMTLATDPTSDNLLACDPGLSRTCDQNIYLSGLCYLIHENLRGPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QKFPEALRGCPQEDSDIAFLVDGSGSIIPHDFRRAKEFISTVMEQLKKSKTLFSLMQYSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          199 YFRTEFTFLDYIKQKDPDALLAGVKHMRLLINTFGAINYVAKEVFRPDLGARPDATKVLI
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   SCNNEDSSLLEDNSATTS-----IPVMYPINVLTKDQENSTLYISFTPKSPRIHHVKH
                                                 OYOV----SNLGQRSLPISLVFLVPVRLNQTVI---WD---RPOVTFS-ENLSSTCHTKE
                                                                              IYOVRIQPSNYDNMP-PLEALVRVPRVHSEGLÍTHKWSIQMEPPVNCSPRNLESPSDEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1166;
                                                                                                                                                                                                                                                                                                                                                                                   02-WAR-2004 (TrEWBLrel. 27, Created)
02-WAR-2004 (TrEWBLrel. 27, Last sequence update)
02-WAR-2004 (TrEWBLrel. 27, Last annotation update)
Lymphocyte function-associated antigen 1 alpha subunit CD11a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dileepan T., Thumbikat P., Kannan M.S., Maheswaran S.K.; "Molecular cloning and sequencing of bovine CD11a."; submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases. EMBL; A7818258; AAQ90015.1; -7 SEQUENCE 1166 AA; 128723 MW; 7BBDBAFBA896C9DF CRC64;
                                                                                                                                                                                                                                                              ITAALYKLGFFKRQYKDMM------SEGGPPGAEPQ 1137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 34.6%; Pred. No. 7.6e-94; nes 409; Conservative 198; Mismatches 469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26.5%; Score 1557; DB 2;
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                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bovidae; Bovinae; Bos.
NCBL_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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AAQ90015;
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Matches
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                                                                                                                                                                                                                                             leukocytes recruitment.
SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-L
SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-L
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: Leukocytes.
DOWAIN: The hitegrin I-domain (insert) is a VWFA domain. Integrins with I-domains do not undergo protease cleavage.
SIMILARITY: Belongs to the integrin alpha chain family.
SIMILARITY: Contains 1 FG-GAP repeats.
SIMILARITY: Contains 1 VWFA domain.
                                                                                                                                              FUNCTION: Integrin alpha-L/beta-2 is a receptor for ICAMI, ICAMI, ICAMZ, ICAM3 and ICAM4. Is involved in a variety of immune phenomena including leukocyte-endothelial cell interaction, cytotoxic T-cell mediated killing, and antibody dependent killing by granulocytes and monocytes. Mice expressing a null mutation of the alpha-L subunit gene demonstrate impaired tumor rejection and impaired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Springer T.A., Teplow D.B., Dreyer W.J.;
"Sequence homology of the LFA-1 and Mac-1 leukocyte adhesion
glycoproteins and unexpected relation to leukocyte interferon.";
Nature 314:540-542 (1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Integrín alpha-L.
Extracellular (Potential).
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FG-GAP 1.
FG-GAP 2.
 alpha-subunit and its expression in COS cells.";
J. Immunol. 147:369-374(1991).
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FG-GAP
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MGD; MGI:96606; Itgal.
InterPro; IPR000413; Integrin_alpha
InterPro; IPR002035; VWF_A.
                                                               MEDLINE=85188276; PubMed=3887182;
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Pfam; PF00357; Integrin_alpha; 1.
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HSSP; P20701; 1DGQ.
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                                                              883 WEDFVELNGTVHCENENSSLQEDNSAATHIPVLYPVNILTKEQENSTLYISFTPKGPKTQ 942
                                                                                                                                            935 VMQHQYQVSNLGQRSLPISLVPLVPVRLNQTVIMDRPQ----VTFSENLSS----TCHTK 986
               876 LGNKLLLLKANVISEN-NMPRINKTEFQLELPVKYAVYMVVISHGVSTKYLNFTASENISR 934
763 DDLSITFSFMSLDCLVVGGP-----REFNVTVTNDGEDSYRTQVTFFFPLDLSYRKV 816
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US-09-902-481B-5 5876 Perfect score:

1 FNLDTENAMTFQENARGFGQ..........FKRQYKDMMSEGGPPGAEPQ 1137 Sednence:

Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table:

2002273 seqs, 358729299 residues Searched:

2002273 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

A\_Geneseq\_23Sep04:\* geneseqp1980s:\* geneseqp1990s:\* geneseqp2000s:\* geneseqp2001s:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp2004s:\* 

|           | script         | Aaw65090 Human Bet | 0        |          | Abq61469 Human Bet | œ        | Ŋ        |          |          | Protei   | Adp44061 Human CD1 |          | Adq17510 Human sof | p150.9   | Aaw65091 Human Bet | Aab07361 Human CD1 | Abg61470 Human Bet | Abu07406 Protein d | Adg32005 Human hom |          | Aaw23049 Human bet | Aaw57491 Human bet | Aaw65089 Human Bet |          | Aaw73342 Human alp | Aab07359 Human alp |
|-----------|----------------|--------------------|----------|----------|--------------------|----------|----------|----------|----------|----------|--------------------|----------|--------------------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|----------|--------------------|--------------------|--------------------|----------|--------------------|--------------------|
| SUMMARIES | Ω              | AAW65090           | AAB07360 | AAU80252 | ABG61469           | AA014428 | ADD25615 | AAR04136 | ADM99589 | ADP12435 | ADP44061           | ADN02004 | ADQ17510           | AAR07120 | AAW65091           | AAB07361           | ABG61470           | ABU07406           | ADG32005           | AAR78166 | AAW23049           | AAW57491           | AAW65089           | AAW72825 | AAW73342           | AAB07359           |
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| d         | Query<br>Match | 99.8               | 8.66     | φ.       | 99.8               | 8.66     |          | 99.6     | 99.5     |          | 59.3               | 59.0     | 59.0               | 58.9     | 58.6               | 58.6               | 58.6               | 58.6               | 58.6               | 58.0     | 58.0               | 58.0               | 58.0               | 58.0     | 58.0               | 58.0               |
|           | Score          | 5862               | 5862     | 86       | 5862               | 5862     | 5862     | Ŋ        | 5846.5   | 5839.5   | 3483               | 3469     | 3469               | 3460     | 3446               | 3446               | 3446               | 3444               | 44                 | 3411     | 3411               | 3411               | 41                 | 3411     | 3411               | 3411               |
|           | Result<br>No.  |                    | 7        | æ        | 4                  | 5        | 9        | 7        | В        | 6        | 10                 | 11       | 12                 | 13       | 14                 | 15                 | 16                 | 17                 | 18                 | 19       | 20                 | 21                 | 22                 | 23       | 24                 | 25                 |

| Abg61468 Human Bet | Aaw23064 Human bet | Aaw65106 Human Bet | Aaw72837 Human alp | Aaw73343 Human alp | Aab07376 Human alp | Abg61485 Human Bet | Aar78169 Rat alpha | Aaw23062 Rat beta | Aaw60004 Rat alpha | Aaw72824 Rat alpha | Aab07374 Rat alpha | Abg61483 Rat Beta2 | Aaw65104 Rat beta- | Aaw73345 Rat alpha | Aaw23061 Mouse bet | Aaw60003 Mouse alp | Aaw65103 Mouse bet | Aaw72836 Mouse alp | Aaw73347 Mouse alp |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| ABG61468           | AAW23064           | AAW65106           | AAW72837           | AAW73343           | AAB07376           | ABG61485           | AAR78169           | AAW23062          | AAW60004           | AAW72824           | AAB07374           | ABG61483           | AAW65104           | AAW73345           | AAW23061           | AAW60003           | AAW65103           | AAW72836           | AAW73347           |
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| 58.0               | 57.8               | 57.8               | 57.8               | 57.8               | 57.8               | 57.8               | 55.0               | 55.0              | 55.0               | 55.0               | 55.0               | 55.0               | 54.9               | 54.9               | 54.8               | 54.8               | 54.8               | 54.8               | 54.8               |
| 3411               | 3395.5             | 3395.5             | 3395.5             | 3395.5             | 3395.5             | 3395.5             | 3234.5             | 3232.5            | 3232.5             | 3232.5             | 3232.5             | 3232.5             | 3225.5             | 3225.5             | 3222               | 3222               | 3222               | 3222               | 3222               |
| 26                 |                    | 28                 | 29                 | 30                 | 31                 | 32                 | 33                 | 34                | 35                 | 36                 | 37                 | 38                 | 39                 | 40                 | 41                 | 42                 | 43                 | 44                 | 45                 |

## ALIGNMENTS

Beta-integrin alpha-d subunit; human; modulator; treatment; psoriasis; type-I diabetes; atherosclerosis; multiple sclerosis; asthma; lung inflammation; acute respiratory distress syndrome; CD11b subunit; rheumatoid arthritis. Human Beta-integrin CD11b subunit protein. AAW65090 standard; protein; 1153 AA. (first entry) 28-SEP-1998 AAW65090; RESULT 1 AAW65090 

Homo sapiens

US5728533-A.

17-MAR-1998

95US-00485618. 07-JUN-1995;

93US-00173497. 94US-00286889. 94US-00362652. 23-DEC-1993; 05-AUG-1994; 21-DEC-1994;

(ICOS-) ICOS CORP.

Gallatin WM; Van Der Vieren M,

WPI; 1998-206565/18.

or Screening assay for modulators of integrin binding - using immobilised o labelled alpha-d polypeptide, useful for, e.g. treating type-I diabetes.

Example 5; Fig 1A-D; 106pp; English.

This sequence represents a human beta-integrin CD11b subunit which is used to describe a method for identifying compounds that modulate the interaction of the beta-integrin alpha-d subunit with a binding partner of alpha-d which involves contacting an alpha-d polypeptide with an alpha-d binding partner, one of which is immobilised and the other of which is labelled, in the presence of a test compound, and determining if the compound affects binding between the alpha-d polypeptide and alpha-d binding partner, where the alpha-d polypeptide is alpha-d or its fragment comparising the cytoplasmic, transmembrane or extracellular domain of alpha-d. Compounds that modulate alpha-d binding could be used to treat

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diseases such as type-I diabetes, atherosclerosis, multiple sclerosis, asthma, psoriasis, lung inflammation, acute respiratory distress syndrome
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in cellular adhesion. Integrins are made up of an alpha subunit and a beta subunit. One class of human integrins are restricted to expression in white blood cells and have a common beta2 subunit: the leukcyte cin white blood cells and have a common beta2 subunit: the leukcyte cintegrins. Leu-CAMS, leukcintegrins or beta2 integrins. Beta2 integrins correctly and manue and inflammatory responses. The present correctly sequence is the human integrin alpha subunit CDILD. This sequence was used in an alignment to identify a novel beta2 integrin alpha combinit; alpha d (AAA60014 and AAB607359). The present sequence has approximately 60% identity to the protein sequence of alpha d. The corporation and protein may be useful in therapy for diseases linked to aberrant alpha d function e.g. Type I diabetes, atherosclerosis, multiple solerosis, asthma, psoriasis, lung inflammation, acute respiratory (LAD). In addition, anti-alpha d monoclonal antibodies may be used in the sistem injury. The monoclonal antibodies can also be used to detect and
                                                                      1080
                                                                                           RINQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDIP 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   macrophage infiltration and reduce inflammation at central nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                        leukocyte integrin, Leu-CAM, leukointegrin, immune response; inflammation, leukocyte adhesion deficiency; LAD, Type I diabetes; atherosclerosis; multiple sclerosis; asthma; psoriasis; beta2 integrin; lung inflammation; aute respiratory distress syndrome; Crohn's disease; rheumatoid arthritis; central nervous system injury; CD11b.
                                                                                                                                             KVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMMSEGGPPGAEPQ 1137
                                                                                                                                                                    KVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMMSEGGPPGAEPQ 1153
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                      RINGTVIMDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDIP
                                                                      FFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLFGQGAFVRSQTET
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system injury. The monocl diagnose Crohn's disease

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Human integrin 1 alpha-M subunit protein.
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This invention relates to a modified integrin-I or integrin I-like domain polypeptide comprising at least one disulfide bond so that the domain is stabilised in a desired conformation. The polypeptide of the invention may have antiinflammatory or imunosuppressive activities. The invention may have antiinflammatory or imunosuppressive activities. The invention may have antiinflammatory or imunosuppressive activities. The invention is manufaction for an integrin a selectively bind to integrin I-commain, and for identifying a modulator of integrin activity, or of interaction of an integrin and a cognate ligand. The polypeptide of the invention, or antibodies (preferably anti-LFA-1 antibody) is useful for treating or preventing an integrin mediated disorder which is an influence of an integrin to a cognate ligand such as Crohn's disease, nephritis; human immunodeficiency virus (HIV), myocardial infarction, Slorgen's syndrome, rheumatoid arthritis, deformatitis. A therapputic composition comprising the peptide of the invention is useful for treating an integrin mediated disorder in a subject. The polypeptide of the invention is useful for and/or artive or anticonic frammate are necking as madiated disorder in a subject. The polypeptide of the invention is useful for and/or artive or anticonic frammate are necking as madiated disorder in a subject.
and/or active or antigenic fragments are useful as reagents for diagnosis of integrin-mediated disorders. The present sequence represents the human integrin.1 alpha-M protein subunit used to generate the mutant polypeptides of the invention
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Beta2 integrin alphaD protein sequences
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Pred. No. 0;
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RLNQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLABLRKAPVVNCSIAVCQRIQCDIP 1036 KVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMMSEGGPPGAEPQ 1137 KVEPPEVPNPLPLIVGSSVGGLILLALITAALYKLGFFKRQYKDMMSEGGPPGAEPO 1153 FFGIOBEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLFGGGAFVRSOTET FFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLPGQGAFVRSQTET Human Beta2 integrin alphaCD11b subunit. Ş

Beta2 integrin; alphaD subunit; CD11c subunit; CD11b subunit; LAD; leukocyte adhesion deficiency; inflammatory response; diabetes; multiple sclerosis; arthritis; diabetes; neuroprotective; inflammatory bowel disease; Crohn's disease; ulcerative colitis; immune complex alveolitis; leukaemia; ICAM-R; VCAM-1; anti-inflammatory; infracellular cell adhesion molecule; vascular cell adhesion molecule; autonomotor recovery; locomotor damage; locomotor impairment; autonomic dysfunction; sensory dysfunction; spinal cord injury.

Use of an anti-alpha-d monoclonal antibodies for promoting locomotor recovery, inhibiting locomotor damage, limiting locomotor impairment, or limiting autonomic and sensory dysfunction following spinal cord injury.

Example 5; Page 191-194; 270pp; English.

The invention relates to promoting locomotor recovery, inhibiting autonomic locomotor damage, limiting locomotor impairment, or limiting autonomic and sensory dysfunction following spinal cord injury by administering an anti-alpha d (Beta2 integrin alpha2 subunit) monoclonal antibody to a canti-alpha d (Beta2 integrin alpha2 subunit) monoclonal antibody to a spinal cord injury victim. The method also involves the use of a ligand conscious of the spinal convolves the use of a ligand condour recovery, inhibiting locomotor damage, limiting locomotor impairment, or limiting autonomic and sensory dysfunction following spinal cord injury. In particular, the spinal cord injury comprises compression of the spinal cord. The antibodies are also useful for reducing inflammation at the site of a central nervous system injury. The specification also details the identification of Beta2 integrin alphaD condous malso details the identification of Beta2 integrins are implicated in diseases such as LAD (leukocyte adhesion deficiency, inflammatory response, diabetes, multiple sclerosis, arthritis, graft the atherosclerosis, inflammatory bowel disease, Crohn's disease, ulcerative and present sequence is a Beta2 integrin alpha subunit sequence included for comparison with the

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Matches 1129; Conservative
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The invention comprises structurally biased variant integrin inserted (I) domain proteins, wherein the alterations to the protein occur in at least two noncontinuous regions. Specifically the the variant integrin I domain proteins are structurally biased to exist in the open conformation, thereby altering the binding ability of the protein. The invention also comprises nucleic acids encoding the variant integrin I domain proteins. The integrin I domain proteins and nucleic acids are useful for treating, preventing or suppressing integrin related inflammatory and immunological storate season and nucleic acids arthritis). The variant integrin I domain or or proteins and nucleic acids can also be used for treating: ischaemia/ reperfusion (e.g. hypovolemic shock); infraction; cerebral shock; viral infection; and cancer. The variant integrin I domain nucleic acids and proteins may be used in gene therapy, as vaccines and to screen for bioactive agents. The present amino acid sequence represents the Mac-1
                                                  1037 FFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTABILFNDSVFTLLPGGGAFVRSQTET 1096
FFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLPGQGAFVRSQTET 1080
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                                                                                                                                                                                                                                                                                                                                                                                                              AAO14428 standard; protein; 1153
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The invention relates to a binding domain-immunoglobulin fusion protein comprising a binding domain polypeptide that is fused to an immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain CH2 constant region polypeptide that is fused to the hinge region polypeptide that is fused to the CH2 constant region polypeptide. The CH2 constant region polypeptide comprises: a wild-type human Igd1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues; where the mutated human Igd1 immunoglobulin hinge contains 2 cysteine residues, where the first cysteine is not mutated; a mutated human Igd1 immunoglobulin hinge region polypeptide mutated human Igd1 immunoglobulin hinge region polypeptide immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues, where the mutated human Igd1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues, where the mutated human Igd1 immunoglobulin hinge region polypeptide contains no more than one immunoglobulin place region polypeptide contains no more than one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cysteine residue; and a mutated human igdl immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues; where the mutated human igdl immunoglobulin hinge region polypeptide contains no cysteine residues. The binding domain-immunoglobulin fusion protein is capable of at least one immunoblogical activity comprising antibody dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    binding domain polypeptide is capable of specifically binding to an antigen. Also included are an isolated polynuclectide encoding the binding domain-immunoglobulin fusion protein, a recombinant expression construct comprising the polynuclectide (operably linked to a promoter), a host cell transformed or transfected with a recombinant expression construct, producing the binding domain-immunoglobulin fusion protein, a
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                                                                                                                                                                                     (first entry)
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          FNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSTGSCEPI
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                                                              RLOVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLRQQPQK
                                                                                                     RLOVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLRQQPQK
                                                                                                                                                  FPEALRGCPQEDSDIAFLVDGSGSIIPHDFRRAKEFISTVMEQLKKSKTLFSLMQYSEEF
                                                                                                                                                                                                                              RIHFTFKEFQNNPNPRSLIKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILILI
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antiarthritic; immunosuppressive; antidiabetic; antithyroid; neuroprotective; hinge region; immunoglobulin heavy chain; CHZ constant region; IgG1, onstant region; EG3 constant region; IgG1, antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New binding domain-immunoglobulin fusion protein, useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, Grave's disease or autoimmune disease.
1097 KVEPPEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQXKDMMSEGGPPGAEPQ 1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Binding domain-immunoglobulin fusion protein-associated protein #85.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma; rheumatoid arthritis; myasthenia gravis; Grave's disease; type I diabetes mellitus; multiple sclerosis; autoimmune disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             domain; immunoglobulin; fusion protein;
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17-JAN-2002; 2002US-00053530.
03-JUN-2002; 2002US-0385691P.
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pharmaceutical composition comprising the binding domain-immunoglobulin fusion protein or polymuclectide and a carrier, and treating a subject having or suspected of having a malignant condition or a B-cell disorder. The binding domain-immunoglobulin fusion protein is useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, carcinoma or sarcoma, rheumatodid arthritis, myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple sclerosis or autoimmune disease. The present sequence is a binding domain-immunoglobulin fusion protein-associated protein sequence. Note: The sequence data for this patent formed part of the printed specification and is also available in electronic format directly from USPTO at sequences in the printed specification bumber therefore none of the sequences can be explicitly identified.

Sequence 1153 AA

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ô 240 256 TDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVN 316 480 540 RLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLRQQPQK 120 TDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTVASKPPRDHVFQIN 300 NFEALKTIONOLREKIFAIEGTOTGSSSSFEHEMSOEGFSAAITSNGPLLSTVGSYDWAG 360 GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR 420 436 496 900 616 9 YDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNF 720 736 780 556 9 16 GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR HGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTVGAQGHVLLLRSQ SLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVG FPEALRGCPQEDSDIAFLVDGSGSIIPHDFRRAKEFISTVMEQLKKSKTLFSLMQYSEEF RIHFTFKEFQNNPNPRSLIKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILILI QNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPL **ONTGMWESNANVKGTOIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGOVSVCPL** PRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLF PRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLF YDIALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNF FNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSTGSCEPI HGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTVGAQGHVLLLRSQ PVLRVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVT Gaps 0 DB 7; Length 1153; 1; Indels 99.8%; Score 5862; D 99.3%; Pred. No. 0; live 7; Mismatches Query Match Best Local Similarity 99.3 Matches 1129; Conservative 377 437 17 61 77 617 121 137 181 197 241 257 301 317 361 481 497 541 557 601 661 677 721 737 421

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| 901 OLELPUXXAVAWAVYSHCAVSTKYIAFTASEBRYSRAWGHQYQVSNLQQRSLPJ 917 OLELPUXXAVAWAVVSHCAVSTKYIAFTASEBRYSRAWGHQYQVSNLQQRSLPJ 917 OLELPUXXAVAYWAVVSHCASTKYIAFTASEBRYSRAWGHQYQVSNLQQRSLPJ 918 ELNOTVIWDRPQYTSEBLSSTCHTKERLPSHSDFLAELERAPVWCSTAVC 1021 FFGIQEEPRATIKGNLSSTCHTKERLPSHSDFLAELERAPVWCSTAVC 1021 FFGIQEEPRATIKGNLSSPWIKTSHHLLIVSTAFLLFNDSYFTLLFQGA 1037 FFGIQEEPRATIKGNLSSPWIKTSHHLLIVSTAFLLFNDSYFTLLFQGA 1037 FFGIQEEPRATIKGNLSSPWIKTSHHLLIVSTAFLLFNDSYFTLFQGASCAPP 1048 KVEPFEVPNPLPLIVGSSVGGLLLALITAALXKLGFFKRQYKDWGSEGGAPP 1059 KVEPFEVPNPLPLIVGSSVGGLLLALITAALXKLGFFKRQYKDWGSEGGAPP 1050 KVEPFEVPNPLPLIVGSSVGGLLLALITAALXKLGFFKRQYKDWGSEGGAPP 1057 KVEPFEVPNPLPLIVGSSVGGLLLALITAALXKLGFFKRQYKDWGSEGGAPP 1057 KVEPFEVPNPLPLIVGSSVGGLLLALITAALXKLGFFKRQYKDWGSEGGAPP 1058 ARCHISC 1057 KVEPFEVPNPLPLIVGSSVGGLLLALITAALXKLGFFKRQYKDWGSEGGAPP 1058 ARCHISC 1057 KVEPFEVPNPLPLIVGSSVGGLLLALITAALXKLGFFKRQYKDWGSEGGAPP 1058 ARCHISC 1058 ARCHISC 1058 ARCHISC 1059 KVEPFEVPNPLPLIVGSSVGGLLLALITAALXKLGFFKRQYKDWGSEGGAPP 1059 KVEPFEVPNPLPLIVGSSVGGLLLALITAALXKLGFFKRQYKDWGSEGGAPP 1051 ARCHISC 1057 KVEPFEVPNPLPLIVGSSVGGLLLALITAALXKLGFFKRQYKDWGSEGGAPP 1051 ARCHISC 1057 KVEPFEVPNPLPLIVGSSVGGLLLALITAALXKLGFFKRQYKDWGSEGGAPP 1051 ARCHISC 1057 KVEPFEVPNPLPLIVGSSVGGLLLALITAALXKLGFFKRQYKDWGSEGGAPP 1051 ARCHISC 1057 KVEPFEVPNPLPLIVGSSVGGLLLALITAALXKLGFFKRQYKDWGSEGGAPP 1051 ARCHISC 1051   | 92 dg            | 4 13                             | SGALK<br>     <br>SGALK | 70  |
| 961 RINOTVINDRPOVTFSENLSSTCHTKERLP 1021 FFGIQEERNATLKGNLSFDWYIKTSHNHLL 1037 FFGIQEERNATLKGNLSFDWYIKTSHNHLL 1037 FFGIQEERNATLKGNLSFDWYIKTSHNHLL 1081 KVEPFEVPNPLPLIVGSSVGGLLLLALITA 1097 KVEPFEVPNPLPLIVGSSVGGLLLLALITA AAR04136; 09-SEP-2004 (revised) 07-SEP-1990 (first entry) Alpha subunit of Mac-1 leukocyte adhesi Mac-1 alpha subunit; Mac-1 alpha/beta h non-specific defence system; integrin g Synthetic.  Key Modified-site 86. 1. 16 Modified-site 87. 1. 16 Modified-site 99. 39. 393 Modified-site 99. 392 Modified-site 697. 699 Modified-site 697. 699 Modified-site 697. 699 Modified-site 697. 699 Modified-site 697. 120 Modified-site 697. 699 Modified-site 697. 699 Modified-site 697. 699 Modified-site 697. 699 Modified-site 697. 699 Modified-site 801. 393 Modified-site 812. 394 Modified-site 812. 394 Modified-site 812. 394 Modified-site 812. 394 Modified-site 812. 394 Modified-site 812. 394 Modified-site 812. 394 Modified-site 812. 394 Modified-site 812. 394 Modified-site 812. 394 Modified-site 812. 394 Modified-site 812. 394 Modified-site 812. 394 Modified-site 812. 394 Modified-site 947. 394 Modified-site 947. 394 Modified-site 947. 394 Modified-site 947. 394 Modified-site 947. 394 Modified-site 947. 394 Modified-site 947. 394 Modified-site 947. 394   | QY               | 0 7                              | OLELE<br>     <br>OLELE | PVKXAVYMVTSHGVSTKYLMFTASENTSRVMQHQYQVSNLGQRSLDISLVFLVPV 96 <br>   |
| 1021 FFGIQEEPNATLKGNLSFDWYIKTSHNHLL 1037 FFGIQEEPNATLKGNLSFDWYIKTSHNHLL 1037 FFGIQEEPNATLKGNLSFDWYIKTSHNHLL 1037 KVEPFEVPNPLPLIVGSSVGGLLLALITA 1057 KVEPFEVPNPLPLIVGSSVGGLLLALITA 1057 KVEPFEVPNPLPLIVGSSVGGLLLALITA 1057 KVEPFEVPNPLPLIVGSSVGGLLLALITA 1057 KVEPFEVPNPLPLIVGSSVGGLLLALITA 1057 KVEPFEVPNPLPLIVGSSVGGLLLALITA 1057 KVEPFEVPNPLPLIVGSSVGGLLLALITA 1057 KVEPFEVPNPLPLIVGSSVGGLLLALITA 1057 KVEPFEVPNPLPLIVGSSVGGLLLALITA 1057 KVEPFEVPNPLPLIVGSSVGGLLLALITA 1057 KVEPFEVPNPLPLIVGSSVGGLLLALITA 1057 KVEPFEVPNPLPLIVGSSVGGLLLALITA 1057 KVEPFEVPNPLPLIVGSSVGGLLLALITA 1057 KVEPFEVPNPLPLIVGSSVGGLLLALITA 1057 KVEPFEVPNPLPLIVGSSVGGLLLALITA 1058 KROJI 107 KVEPFEVPNPLPLIVGSSVGGLLLALITA 1058 KROJI 107 KVEPFEVPNPLPLIVGSSVGGLLLALITA 1058 KROJI 107 KVEPFEVPNPLPLIVGSSVGGLLLALITA 1058 KROJI 1058 KROJI 1058 KROJI 1058 KROJI 1058 KROJI 1059 KVEPFEVPNPLPLIVGSSVGGLLLALITA 1059 KROJI 1050 1050 1050 1050 1050 1050 1050 1050  | ογ               | 9                                | RLNOT                   | SHSDFLAELRKAPVVNCSIAVCQRIQCDIP 1                                  |
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| 1081 KVEPFEVPNPLPLIVGSSVGGLLLALITAALYKLGFFKRQYKDWASEGGPPGAEP 1097 KVEPFEVPNPLPLIVGSSVGGLLLALITAALYKLGFFKRQYKDWASEGGPPGAEP 3436 3436 34864136 standard; protein; 1153 AA. AAR04136 standard; protein; 1153 AA. AAR04136; 09-SEP-2004 (revised) 25-MAR-2003 (first entry) Alpha subunit of Mac-1 leukocyte adhesion receptor. Mac-1 alpha subunit; Mac-1 alpha/beta heterodimer; Monor specific defence system; integrin gene superfamily. Synthetic.  Key 1. 16 Modified-site (Jabel= signal_peptide Modified-site (Jabel= putative N-glycosylation site Mo  | S d              | 02                               | FGI                     | DEEFNATLKGNLSFDWYIKT<br>  |
| AARO4136 standard; protein; 1153 AA.  AARO4136;  09-SEP-2004 (revised) 07-SEP-1990 (first entry)  Alpha subunit of Mac-1 leukocyte adhesion receptor.  Mac-1 alpha subunit; Mac-1 alpha/beta heterodimer;  non-specific defence system; integrin gene superfamil Synthetic.  Key  Location/Qualifiers  Region  1.abel = putative N-glycosylation site Modified-site 450. 242  Alabel = putative N-glycosylation site Modified-site 693. 695  Modified-site 693. 695  Modified-site 693. 695  Modified-site 693. 695  Modified-site 693. 695  Modified-site 693. 695  Modified-site 693. 695  Modified-site 802. 804  Modified-site 802. 804  Modified-site 802. 804  Modified-site 802. 804  Modified-site 802. 804  Modified-site 803. 904  Modified-site 803. 904  Modified-site 803. 904  Modified-site 803. 904  Modified-site 803. 904  Modified-site 991. 903  Modified-site 991. 903  Modified-site 941. 943  Modified-site 941. 943  Modified-site 941. 943  Modified-site 941. 943  Modified-site 941. 943  Modified-site 941. 943  Modified-site 941. 943  Modified-site 941. 943  Modified-site 941. 943  Modified-site 941. 943  Modified-site 941. 943  Modified-site 941. 943  Modified-site 941. 943  Modified-site 941. 943  Modified-site 941. 943  Modified-site 941. 943  Modified-site 941. 943  Modified-site 941. 943  Modified-site 941. 943   | Qy<br>Qu         | 90                               | KVEPF<br>     <br>KVEPF | ?KRQYKDMMSEGGPPGAEP<br>   |
| AARO4136; 09-SEP-2003 (revised) 25-MAR-2003 (revised) 07-SEP-1990 (first entry) Alpha subunit of Mac-1 leukocyte adhesion receptor. Mac-1 alpha subunit; Mac-1 alpha/beta heterodimer; non-specific defence system; integrin gene superfamil Synthetic.  Key  Location/Qualifiers Region  1. 16 Modified-site 86. 88 Modified-site 740. 242 Alabel putative N-glycosylation site 740. 242 Alabel putative N-glycosylation site 740. 391 Modified-site 69. 471 Modified-site 697. 699 Modified-site 697. 699 Modified-site 697. 699 Modified-site 735. 737 Alabel putative N-glycosylation site 735. 737 Alabel putative N-glycosylation site 802. 804 Modified-site 735. 737 Alabel putative N-glycosylation site 802. 804 Modified-site 901. 903 Modified-site 912. 914 Modified-site 913. 934 Modified-site 913. 934 Modified-site 913. 934 Modified-site 913. 934 Modified-site 913. 934 Modified-site 914. 943 Modified-site 917. 949 Modified-site 947. 949 Modified-site 947. 949 Modified-site 947. 949 Modified-site 947. 949 Modified-site 947. 949 Modified-site 947. 949 Modified-site 947. 949 Modified-site 947. 949 Modified-site 947. 949 Modified-site 947. 949   | RES<br>AAR<br>ID | JLT 7<br>24136<br>AAR0413        | t)                      | ard; protein; 1153  |
| 09-5EP-2004 (revised) 25-MAR-2003 (revised) 07-SEP-1990 (first entry) Alpha subunit of Mac-1 leukocyte adhesion receptor. Mac-1 alpha subunit; Mac-1 alpha/beta heterodimer; non-specific defence system; integrin gene superfamil synthetic.  Key 10.16 Alabel = putative N-glycosylation site Modified-site (1abel = putative N-glycosylation site (1abel = putative N-glycosyl  | AC               | AAR04136                         | ••                      |   |
| Alpha subunit of Mac-1 leukocyte adhesion receptor.  Mac-1 alpha subunit; Mac-1 alpha/beta heterodimer;  non-specific defence system; integrin gene superfamil Synthetic.  Key  Location/Qualifiers  1. 16  Modified-site   Jabel   | Z E E E          | 09-SEP-2<br>25-MAR-2<br>07-SEP-1 | 44 W C                  | <pre>(revised) trevised) (first entry)</pre>                      |
| Mac-1 alpha subunit; Mac-1 alpha/beta heterodimer; non-specific defence system; integrin gene superfamil Synthetic.  Location/Qualifiers  Region    1.06  | X H :            | Alpha                            | ounit                   | Mac-1 leukocyte adhesion recepto                                  |
| Synthetic.  Key  1. 16  Alabel= signal_peptide  86. 88  Alabel= putative N-glycosylation sit  1. 30. 1303  Alabel= putative N-glycosylation sit  Modified-site  1. 30. 471  Modified-site  693. 693  Modified-site  693. 693  Modified-site  735. 737  Modified-site  735. 737  Modified-site  736. 994  Modified-site  736. 904  Modified-site  737. 138  Modified-site  738. 139  Modified-site  739. 1803  Modified-site  730. 1803  Modified-site  731. 1803  Modified-site  732. 1804  Modified-site  733. 1803  Modified-site  734. 1803  Modified-site  735. 1914  736. 1914  736. 1914  736. 1914  737. 1949  Modified-site  738. 1943  Modified-site  739. 1944  Modified-site  739  | ŽŽŽį             | Mac-1 al<br>non-spec             | w . d                   | Mac-1 alpha/beta heterodimer;<br>system; integrin gene superfamil |
| Region  1. 16  Modified-site  Modifi  | SO S             | Syntheti                         | Ö                       |   |
| Modified-site 86.88  / Jabel= signal_peptide  Modified-site 740242  / Jabel= putative N-glycosylation sit  / Jabel= putative N-glycosylation sit  Modified-site 713.93  / Jabel= putative N-glycosylation sit  / Modified-site 693695  Modified-site 693695  / Jabel= putative N-glycosylation sit  / Jabel= putative N-glycosyla   | X E E            |                                  |                         | Ä   |
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integrin alpha subunit, beta, antipsoriatic; thrombolytic; anticoagulant; osteopathic; cytostatic; immunosuppressive; antiinflammatory; europrotective; antisickling; immunotherapy; inflammatory; autoimmune disorder; thrombosis; cancer; osteoporosis; sickle cell anaemia; psoriasis; multiple sclerosis; human; precursor;
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                                         QNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPL
                                                                                                          PRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLF
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994. .996
/label= putative N-glycosylation site
1022. .1024
/label= putative N-glycosylation site
1045. .1047
/label= putative N-glycosylation site
1051. .1053
/label= putative N-glycosylation site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA - useful
                                                                                                                                              1076. .1078
/labbel= putative N-glycosylation site
1106. .1134
/label= putative_transmembrane_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New pure Mac-1 alpha sub-unit and corresp. DNA - use inflammation and viral infections, and in diagnosis
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Pred. No. 0;
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89US-00321239.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1153 AA;
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   Modified-site
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09-MAR-1989;
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Matches 1128;
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RINQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDIP 1020
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                                GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR
                                                                               ONTGMWESNANVKGTOIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPL
                                                                                                                                                                                                                                                                       HGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTVGAQGHVLLLRSQ
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      GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR
                                                                                                                     QNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPL
                                                                                                                                                              PRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLF
                                                                                                                                                                                                  PRG-RARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLF
                                                                                                                                                                                                                                         HGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTVGAQGHVLLLRSQ
                                                                                                                                                                                                                                                                                                                    PVLRVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a novel isolated or recombinant modified integrin protein having extracellular domains of integrin alpha and beta subunits where one of the subunits has one or more mutations, an altered surface feature or an amino acid substitution or internal deletion, extracellular domains of the integrin beta subunit that comprise a mutation that alters a non-cysteine residue to cysteine or extracellular domains of integrin alpha and beta subunits. The polypeptide of the invention demonstrates antipsoriatic, thrombolytic, anticoagulant, osteopathic, cytosteatic, immunosuppressive, antiinflammatory, neuroprotective and antisickling activities and may be useful for immunotherapy in order to prevent or treat an integrin-mediated disorder such as an inflammatory disorder, an autoimmune disorder, thrombosis, cancer, osteoporosis, sickle cell anaemia, psoriasis and multiple subunit precursor protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                         Novel modified integrin protein having extracellular domains of integrin alpha and beta subunits or integrin alphaII and beta3 subunit, useful for treating integrin mediated disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEF 196
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Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 4; 232pp; English.
                                    /note= "Encoded by CCC"
Location/Qualifiers
                                                                                                                                                                                          2002US-0396783P.
2002US-0396790P.
2002US-0410135P.
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                                                                                                                                                                                                                                                                       BLOOD RES INC.
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Key
Misc-difference
                                                                           WO2004007530-A2
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                                                                                                               22-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inhibitor; HIV infection; human; CD11C; integrin alpha X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMMSEGGPPGAEPQ 1137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KVEPFEVPNPLPLIUGSSVGGLLLLALITAALYKLGFFKRQYKDMMSEGGPPGAEPQ 1152
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HGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTVGAQGHVLLLRSQ
                              HGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTWDGLVDLTVGAQGHVLLLRSQ
                                                                           PVILRVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRDRIREGQIQSVVT
                                                                                                     YDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNF
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N-PSDB; ADP44060.
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                                                                                                                                                                                               Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in an individual, comprises detecting the expression level of
                                                                                                                                                                                                                                                                                                                                 The present invention relates to diagnosing or monitoring transplant rejection, e.g. cardiac or kidney transplant rejection, in an individual comprises detecting the expression level of one or more genes. The methods, system and kits are useful in diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, aenotransplant rejection or mechanical organ replacement rejection, in an individual. The method is also useful in assessing the immune status of an individual. The methods are also useful in diagnosing and monitoring diseases that involve the immune system, e.g. rheumatoid arthritis, lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or viral, bacterial or fungal infection. The present sequence represents a protein that is encoded by the mRNA of the invention.
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Pred. No. 0;
7; Mismatches
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99.1%;
      2002US-00131831
2002US-00325899
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Matches 1127; Conservative
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                                                                                                     Wohlgemuth J,
      24-APR-2002;
20-DEC-2002;
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The present invention describes a method (M1) for identifying an inhibitor of HIV entry into a human host cell. (M1) comprises identifying an inhibitor of a cell surface polypeptide selected from CXCR-4 (352 amino acids, SEQ ID NO:8, ADP4405), CCR4 (360 amino acids, SEQ ID NO:14, ADP44061), CD47 (323 amino acids, SEQ ID NO:14, ADP44061), CD47 (323 amino acids, SEQ ID NO:14, ADP44063), CD68 (354 amino acids, SEQ ID NO:16, ADP44063), CD78 (335 amino acids, SEQ ID NO:16, ADP44063), CD78 (336 amino acids, SEQ ID NO:20, ADP44067), CD74 (566 amino acids, SEQ ID NO:20, ADP44067), CD74 (566 amino acids, SEQ ID NO:20, ADP44073), CBMBRI (578 amino acids, SEQ ID NO:22, ADP44077), PARA (462 amino acids, SEQ ID NO:32, ADP44077), PARA (462 amino acids, SEQ ID NO:32, ADP44077), PARA (462 amino acids, SEQ ID NO:32, ADP44077), PARA (462 amino acids, SEQ ID NO:32, ADP44077), CTREAL (150 amino acids, SEQ ID NO:30, ADP44077), CTREAL (150 amino acids, S ģ a human host cell useful for preventing and/or treating HIV infection, identifying an inhibitor of a cell surface polypeptide such as CXCR-4. exemplification of the present invention English SEQ ID NO 14; 133pp; 

Sequence 1163 AA;

RLOVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLRQQPQK 120 197 480 540 FPEALRGCPQEDSDIAFLVDGSGSIIPHDFRRAKEFISTVMEQLKKSKTLFSLMQYSEEF 180 TDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTVASKPPRDHVFQIN 300 DFDALKDIQNQLKEKIFAIEGTETTSSSSFELEMAQEGFSAVFTPDGPVLGAVGSFTWSG 377 541 HGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTVGAQGHVLLLRSQ 600 9 79 FNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSTGSCEPI RIHFTFKEFONNPNPRSLIKPITOLLGRIHTATGIRKVVRELFNITNGARKNAFKILILI GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR PRGWR-RWWCDAVLYGEQGHPWGRFGAALTVLGDVNGDKLTDVVJGAPGEEENRGAVYLF NFBALKTIQNQLREKIFAIEGTQTGSSSSFEHEMSQEGFSAAITSNGPLLSTVGSYDWAG PRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLF QNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPL Gaps 9 Length 1163; Query Match 59.3%; Score 3483; DB 8; Length 1 Best Local Similarity 61.2%; Pred. No. 1e-281; Matches 691; Conservative 141; Mismatches 291; Indels 20 80 138 181 301 438 61 121 241 318 361 378 421 481 a g qq g à ŏ δ g qq g ò 셤 ò à à ò à ð

VRINQTVIWDRPQVIFSENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDI 1019 PFFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLPGQGAFVRSQTE 1079 616 099 929 720 736 780 964 840 QLELPVKYAVYMVVTSHGVSTKYLNFTAS-ENTSRVMQHQYQVSNLGQRSLPISLVFLVP 959 854 SQGTWSTSCRINHLIFRGGAQITFLATFDVSPKAVLGDRLLLTANVSSENNTPRTSKTTF 914 marker gene; inflammatory bowel disease; IBD; FcgammaR IIIa; FcgammaR IIIb; Mig; NRG-2; hexokinase; HM74; REG III; LPAP; Mip-1(beta); L-selectin; EGFL6; IDO; IL-8; CD11c; TLR2; ulcerative colitis; Novel marker gene of inflammatory bowel disease (IBD) comprising base sequence of e.g., Fc gamma R IIIa, Fc gamma R IIIb, Mig, NRG-2, hexokinase 3, HM74, CD11c, TLR2 gene, useful for screening therapeutic 677 LDLALDPGRLSPRATFQETKNRSLSRVRVLGLKAHCENFNLLLPSCVEDSVTPITLRLNF PVLRVKAIMEFNPREVARNVFECNDOVVKGKBAGEVRVCLHVQKSTRDRLREGQIQSVVT YDLALDSGRPHSRAVFNETKOSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNF SLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVG GPREFNVTVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEV SNLELNAEVMVWNDGEDSYGTTITFSHPAGLSYRYVAEGOKOGOLRSLHLTCDSAPVG--QLELPVKYAVYTVVSSHEQFTKYLNFSESEEKESHVAMHRYQVNNLGQRDLPVSINFWVP SGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRTNKTEF TKVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMMSE 1128 Human inflammatory bowel disease marker - CD11c protein. Z ADN02004 standard; protein; 1163 07-AUG-2002; 2002JP-00229705 07-AUG-2002; 2002JP-00229705. (first entry) SUMU ) SUMITOMO SEIYAKU WPI; 2004-209124/20. N-PSDB; ADN01990. JP2004065120-A. Homo sapiens 17-JUN-2004 04-MAR-2004 601 617 199 721 737 781 797 841 855 901 915 096 975 1020 ADN02004; Crohn's ADN02004 RESULT à g 셤 à 셤 ò g à à 셤 ò g g q THE STATE OF THE S à ð g à

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which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarched of the invention has cytostatic applications and may be useful for detecting soft tissue sarched, possibly via gene therapy or vaccine production. The nucleic sarched sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma upregulated protein of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.
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                                                 disease (IBD)
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                                              The invention comprises marker genes for inflammatory bowel disease (IBI - FcgammaR IIIa, FcgammaR IIIb, Mig, NRG-2, hexokinase, HM74, REG III, LDAP, Mip-1(bbta), L-selectin, EGFL6, IDO, IL-8, CUILC, and TLR2 genes. The DNA and protein sequences of the invention are useful in the detection and treatment of IBD (e.g. ulcerative colitis and Crohn's disease). The present amino acid sequence represents an IBD marker
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                          27; 151pp; Japanese.
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protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sarcoma; cytostatic; gene therapy; vaccine; screening; human
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                                                                                                                                                                                              VRLNQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDI
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                                               SQGTWSTSCRINHLIFRGGAQITFLATFDVSPKAVLGDRLLLTANVSSENNTPRTSKTTF
                                                                                                 QLELPVKYAVYMVVTSHGVSTKYLNFTAS-ENTSRVMQHQYQVSNLGQRSLPISLVFLVP
                                                                                                                             PFFCIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTARILFNDSVFTLLPGQGAFVRSQTE
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p150,95 leucocyte adhesion receptor alpha-subunit; hairy cell leukaemia;
rhinovirus.
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                               TKVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKROYKDMMSE 1128
                                           TYLEKYKVHNPTPLIVGSSIGGLILLALITAVLYKVGFFKRQYKEMMEE 1143
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Clone lambda X47 was isolated from a cDNA library constructed from total RNA extracted from phosbol myristate acetate stimulated HL-60 myelomonocytic cells. The library was screened with oligonucleotide probes based on tryptic peptide fragments of p150.95. The sequence can be attached to appropriate control elements and expressed in prokaryotic and eukaryotic cells. The protein can be used to treat or prevent rhinoviral infection because it interacts with ICAM-1 and inhibits cell-virus attachment. It can also be used as an anti-inflammatory agent. See also AAQ06063-4, AAR07121-8 and AAR07152-6. (Updated on 25-MAR-2003 to correct PR field.)
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                                                                                                                                                                                                                                                                  61 RLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLRQQPQK
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                                                                                                                                                                  Length 1163;
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%; Pred. No. 8.7e-280;
141; Mismatches 295;
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60.9%;
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This sequence represents a human beta-integrin CDIIc subunit which is used to describe a method for identifying compounds that modulate the interaction of the beta-integrin alpha-d subunit with a binding partner of alpha-d which involves contacting an alpha-d polypeptide with an alpha-d binding partner, one of which is immobilised and the other of which is labelled, in the presence of a test compound, and determining if the compound affects binding between the alpha-d polypeptide and alpha-d binding partner, where the alpha-d polypeptide is alpha-d or its fragment comprising the cytoplasmic, transmembrane or extracallular domain of alpha-d is comprising the cytoplasmic, transmembrane or extracallular domain of alpha-d is comprised that modulate alpha-d binding could be used to treat diseases such as type-I diabetes, atherosclerosis, multiple sclerosis, asthma, psoriasis, lung inflammation, acute respiratory distress syndrome
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labelled alpha-d polypeptide, useful for, e.g. treating type-I diabetes.
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                                                                                                                                             PFFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLPGQGAFVRSQTE
SGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRTNKTEF
                   VRINQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDI
                                                            QLELPVKYAVYMVVTSHGVSTKYLNFTAS-ENTSRVMQHQYQVSNLGQRSLPISLVFLVP
                                                                                                                                                                                                                                                  1080 IKVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMMSE 1128
                                                                                                                                                                                                                                                                    Human Beta-integrin CD11c subunit protein
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94US-00362652.
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and rheumatoid arthritis
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05-AUG-1994;
21-DEC-1994;
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                          Length 1163;
                                              Indels
                       58.6%; Score 3446; DB 2; 60.8%; Pred. No. 1.3e-278;
                                             Conservative 147; Mismatches 290;
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Best Local Similarity
 Sequence 1163 AA;
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Integrins are a class of membrane-associated molecules that participate in cellular adhesion. Integrins are made up of an alpha subunit and a beta subunit. One class of human integrins are restricted to expression in white blood cells and have a common beta2 subunit: the leukocyte integrins, Leu-CAMS, leukointegrins or beta2 integrins. Beta2 integrins con an important role in immune and inflammatory responses. The present control in a lignment to integrin alpha subunit (D11c. This sequence was used in an alignment to identify a novel beta2 integrin alpha as used in an alignment to identify a novel beta2 integrin alpha captroniately 68 identity to the protein sequence of alpha d. The captroniately 68 identity to the protein sequence of alpha d. The Alpha d gene and protein may be useful in therapy for diseases linked to aberrant alpha d function e.g. Type I diabetes, atherosclerosis, multiple constructs as syndrome, rheumatoid arthritis and leukocyte adhesion deficiency (LAD). In addition, anti-alpha d monoclonal antibodies may be used in the system injury. The monoclonal antibodies can also be used to detect and
 PFFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLPGQGAFVRSQTE 1079
                    system
                                                                                                                                                                                                                                                                                                              Human; macrophage infiltration inhibition; alpha_d integrin; leukocyte integrin; Leu-CAM; leukointegrin; immune response; inflammation; leukocyte adhesion deficiency; LAD; Type I diabetes; atherosclerosis; multiple sclerosis; asthma; psoriasis; beta2 integrin; lung inflammation; acute respiratory distress syndrome; Crohn's disease; rheumatoid arthritis; central nervous system injury; CD11c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       monoclonal antibodies to inhibit inflammation at central nervous
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                                                                                    Score 3446; DB 3;
Pred. No. 1.3e-278;
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                FNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSTGSCEPI
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Search completed: November 9, 2004, 12:08:24 Job time: 108.25 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|    |        | Description     | Segment & endemoner | Semience 3 April | Semience 1 Aproli | Semience 3. Appli | Semience 30. April | Semience 176 Ann  | Semience 6. Annli | Seminary A sometimes | Sections 4 brain | Segmence 3. Appli | Semi-pro-         | Semience 4 Appli | Sequence 4, Appli |
|----|--------|-----------------|---------------------|------------------|-------------------|-------------------|--------------------|-------------------|-------------------|----------------------|------------------|-------------------|-------------------|------------------|-------------------|
|    |        | qi              | US-09-902-481A-5    | US-09-350-259-3  | US-09-902-481A-1  | US-09-891-943-3   | US-10-144-259-30   | US-10-207-655-176 | US-09-902-481A-6  | US-09-902-481A-4     | US-09-945-265-4  | US-09-902-481A-3  | US-10-116-275-204 | US-09-350-259-4  | US-09-891-943-4   |
|    |        | gth DB          | 137 10              | 153 9            | 153 10            | 1153 10           | 153 14             | 153 14            | 137 10            | 137 10               | 152 9            | 137 10            | 163 14            | 163 9            | 163 10            |
| ф. | Query  | Match Length DB |                     | 99.8             |                   | 99.8              |                    |                   |                   |                      |                  |                   |                   |                  |                   |
|    |        | Score           | 5876                | 5862             | 5862              | 5862              | 5862               | 5862              | 5855              | 5851                 | 5846.5           | 5836              | 3469              | 3446             | 3446              |
|    | Result | No.             | 1                   | 2                | 3                 | 4                 | Ŋ                  | 9                 | 7                 | 80                   | Đ                | 10                | 11                | 12               | 13                |

| (7)  | Sequence 2, Appl                    | ١٥       | 5    |      | 53               | Sequence 53, Appl | 37.              | 37.              | 46   | 46,       | 121         | 2. App          | ٦.     | Sequence 295, App | Sequence 1871, Ap   | Sequence 103, App | Sequence 103, App | Sequence 2, Appli | 7            | 10                | 9 101      | 103            | 103        | 25(              | 25(          | 81(  | 338          | 35,          | 35,          | 4               |
|------|-------------------------------------|----------|------|------|------------------|-------------------|------------------|------------------|------|-----------|-------------|-----------------|--------|-------------------|---------------------|-------------------|-------------------|-------------------|--------------|-------------------|------------|----------------|------------|------------------|--------------|------|--------------|--------------|--------------|-----------------|
| 09-3 | US-09-891-943-2<br>US-09-350-259-99 | 891-943- |      | 9    | US-09-350-259-53 | US-09-891-943-53  | US-09-350-259-37 | US-09-891-943-37 | 6    | US-09-891 | US-10-087-1 | US-09-945-265-2 | US-10  |                   | US-10-408-765A-1871 | -350-             | US-09-891-943-    | US-10-17          | US-10-173-55 | US-09-350-259-101 | US-09-891- | US-09-984-130- | US-09-836- | US-09-918-715-25 | US-10-474-79 |      | US-10-291-26 | US-09-984-13 | US-09-836-35 | US-10-262-839-4 |
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| •    | 57.8                                |          | 5    | Ď.   | 4                | 54.8              | 4.               | 54.7             | 54.5 | 54.5      | 31.4        | 26.5            | 26.4   | 26.0              | 23.1                | 20.9              | 20.9              | 19.6              | 19.6         | 19.6              | 19.6       | 18.8           | 18.8       | 18.8             | 18.8         | 18.7 | 18.7         | 18.6         | 18.6         | 18.6            |
| 3411 | າຄ                                  | 3395.5   | 232. | ď    | 3222             | 3222              | 3211.5           | 3211.5           | 3201 | 3201      | 1848        | 1557.5          | 1553.5 | 1530              | 1359.5              | 1229.5            | 1229.5            | 1153              | 1153         | •                 | _          | 1103.5         | 1103.5     | 1103.5           | 1103.5       | 1101 | 1097         | 1093.5       | 1093.5       | 1093.5          |
| 14   | 16                                  | 17       | 18   | 19   | 20               | 21                | 22               | 23               | 24   | 25        | 26          | 27              | 28     | 29                | 30                  | 31                | 32                | 33                | 34           | 35                | 36         | 37             | 38         | 39               | 40           | 41   | 42           | 43           | 44           | 45              |

## ALIGNMENTS

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                                                                                       APPLICANT: Spiringer, Timothy
APPLICANT: Shimaoka, Motomu
APPLICANT: Shimaoka, Motomu
APPLICANT: Shiman, Julia
APPLICANT: Shiman, Julia
APPLICANT: Mayo, Stephen
TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
FILE REFERENCE: A-70586-1/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/902, 481A
CURRENT FILING DATE: 2001-07-09
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 2000-07-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO SE
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                     ; Sequence 5, Application US/09902481A; Publication No. US20030054440A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: synthetic
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Best Local Similarity
US-09-902-481A-5
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| Sedication No. US20030109691A1
| Fublication No. US20030109691A1
| GENERAL INFORMATION:
| APPLICANT: Arnaout, M. Amin
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| APPLICANT: Arnaout, M. Amin
| APPLICANT: Arnaout, M. Amin
| FILE REFERENCE: 00766-548001
| CURRENT APPLICATION NUMBER: US 09/758,493
| PRIOR FILING DATE: 2001-01-11
| PRIOR FILING DATE: 2000-07-31
| NUMBER OF SEQ ID NOS: 30
| SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                 GPREFNUTUTURNDGEDSYRTQUTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEV
                                                                                                                      GPREFNVIVIVIVINDGEDSYRIQVIFFFFLDLSYRKVSTLQNQRSQRSWRLACESASSTEV
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99.3%; Pred. No. 0;
:ive 7; Mismatches
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Best Local Similarity 99.33
Matches 1129; Conservative
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CRGANISM: Homo sapiens
US-10-144-259-30
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US-10-144-259-30
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                   APPLICANT: Gallatin, Michael W.
APPLICANT: Callatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. US20030077278Alel Human 2
FILE REPERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/891,943
CURRENT FILING DATE: 1998-11-16
PRIOR APPLICATION NUMBER: 08/286,889
PRIOR FILING DATE: 1994-08-05
PRIOR PLING DATE: 1994-12-21
PRIOR APPLICATION NUMBER: 08/362,652
PRIOR PLING DATE: 1994-12-21
PRIOR PLING DATE: 1994-10-03
PRIOR FILING DATE: 1994-12-21
PRIOR FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE PATENTIN Ver. 2.0
SEQ ID NO SECTION VER. 2.0
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          GENERAL INFORMATION:
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Best Local Similarity 99.3%;
Matches 1129; Conservative sapiens TYPE: PRT ORGANISM: Homo ; ORGANISM: HOUR US-10-207-655-176 LENGTH: 1153 17 17 61 121 181 197 241 301 377 421 437 481 497 541 557 617 677 361 601 199 737 721 841 797 857 781 ò g ð Ωp à qq  $\delta$ qq à qq Db ð ₩ 6 8 6 ò g  $\delta$ qq à qq à 셤 ò g ò g g õ 1020 300 316 360 099 676 256 376 420 436 480 496 540 556 600 616 720 736 780 796 840 856 900 916 RIHFTFKEFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVI

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        QNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPL
                            421 QNTGMWESNANVKGTQIGAXFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPL
                                                                       PRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLF
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APPLICANT: Shimacka, Motomu
APPLICANT: Shimacka, Motomu
APPLICANT: Shimacka, Motomu
APPLICANT: Shiman, Julia
APPLICANT: Mayo, Stephen
TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
FILE REPERENCE: A-70586-1/RFYRMS/RMK
CURRENT APPLICATION NUMBER: US 60/902,481A
CURRENT PILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/216,600
PRIOR FILING DATE: 2000-07-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
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ORGANISM: Artificial sequence
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                    QLELDVKYAVYMVVTSHGVSTKYLNFTASENTSRVMQHQYQVSNLGQRSLPISLVFLVPV
                                                                                   FNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSTGSCEPI
QLELPVKYAVYMVVTSHGVSTKYLNFTASENTSRVMQHQYQVSNLGQRSLPISLVFLVPV
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                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/09902481A

publication No. US20030054440A1

publication No. US20030054440A1

GENERAL INFORMATION:

APPLICANT: Sprimacka, Motomu

APPLICANT: Shimacka, Motomu

APPLICANT: Shimacka, Julia

APPLICANT: Shimacka, Julia

APPLICANT: Mayo, Stephen

TILLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY

FILE REFERENCE: A-70886-1/RFT/RMS/RMK

CURRENT FILING DATE: 2001-07-09

PRIOR PILING DATE: 2001-07-09

PRIOR PILING DATE: 2000-07-07

NUMBER OF SEQ ID NOS: 7

SOFTWARE: Patentin version 3.1
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Pred. No. 0;
8; Mismatches 2;
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Matches 1127; Conservative
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US-09-902-481A-6
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LENGTH: 1137
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US-09-902-481A-6
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                                                                  FFGIOEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLPGGGAFVRSQTET
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                                                                                                                                                                                                                                                                                                                              99.5%; Score 5846.5;
99.2%; Pred. No. 0;
ive 7; Mismatches
                                                                                                                       Sequence 4, Application US/09945265; Patent No. US20020123614A1; GENERAL INFORMATION:
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Matches 1128; Conservative
                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
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                        Length 1137;
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                                         Mismatches
                     Score 5851;
Pred. No. 0;
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                   99.6%;
                 Query Match
Best Local Similarity 99.3
Matches 1129; Conservative
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| 1035 PSFSVQBELDPTLKGNLSFGWVRQILQKKVSVVSVAEITFDTSVYSQLPGQBAFMRAQTT 1094
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                    SLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVG
YDLALDSGRPHSRAVFNETKNSTRROTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNF
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Sequence No. US20020062008A1
GENERAL INFORMATION:
APPLICANT: GAllatin, Michael W.
APPLICANT: GAllatin, Michael W.
TITLE OF INVENTION: No. US20020062008Alel Human 2
FILE REFERENCE: 27866/3500
CURRENT FALLING DATE: 1999-07-08
EARLIER APPLICATION NUMBER: US/09/350,259
CURRENT FILING DATE: 1999-11-16
EARLIER APPLICATION NUMBER: 08/173,497
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SEQ ID NO 4
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60.8%; Pred. No. 1.8e-283;
clve 147; Mismatches 290;
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ORGANISM: Homo
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                                                                       APPLICANT: Blan Pharmaceutical Technology
APPLICANT: Blan Pharmaceutical Technology
APPLICANT: O'Mahony, Daniel J.
APPLICANT: Brayden, David
APPLICANT: Brayden, David
APPLICANT: Brayden, David
APPLICANT: Lambkin, Inelda
APPLICANT: Lambkin, Inelda
APPLICANT: Lambkin, Inelda
APPLICANT: Higgins, Lisa
TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cells and Methods and
TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
CURRENT APPLICATION NUMBER: US/10/116,275
CURRENT FILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 349
SOFTWARE: PatentIn Version 3.1
SEQ ID NO 204
TENATURE: ALLOS 204
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59.0%; Score 3469; DB 14;
Best Local Similarity 61.0%; Pred. No. 2e-285;
Matches 689; Conservative 141; Mismatches 293;
                               Sequence 204, Application US/10116275
Publication No. US20030211476A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
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                                                            RIHFTFKEFQNNPNPRSLIKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILILI
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APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
APPLICANT: Van der Vieren, Monica
TILLE OF INVENTION: NO. US20030077278Alel Hum
FILE REFERENCE: 27866/35004
CURRENT APPLICATION UNMERE: 09/193,043
PRIOR FILING DATE: 1999-1-1-16
PRIOR FILING DATE: 1999-1-1-6
PRIOR FILING DATE: 1999-1-1-2
PRIOR FILING DATE: 1994-08-05
PRIOR FILING DATE: 1994-08-05
PRIOR FILING DATE: 1994-08-05
PRIOR FILING DATE: 1994-08-05
PRIOR FILING DATE: 1994-08-05
PRIOR FILING DATE: 1994-08-05
NUMBER OF SEQ ID NOS: 114
SEQ ID NO 4: 2.0 ORGANISM: Homo sapiens 617 g  $\delta$ 

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Sequence 4, Application US/09891943

RESULT 13 US-09-891-943-4

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Publication No. US20030077278A1
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US-09-891-943-2
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APPLICANT: Gallatin, Michael W.
TITLE OF INVENTION: No. US20020062008Alel Human 2
FILE REPERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/350,259
CURRENT FILING DATE: 1999-07-08
EARLIER APPLICATION NUMBER: 09/193,043
EARLIER FILING DATE: 1999-11-16
EARLIER FILING DATE: 1999-11-23
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
CONTWARE: PATCHIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 2, Application US/09350259; Patent No. US20020062008A1; GENERAL INFORMATION;
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Best Local Similarity 59.4%; Pred. No. 1.7e-280;
Matches 671; Conservative 166; Mismatches 284;
                      N
                      Human
APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. US20030077278Alel Hum
FILE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/891,943
PRIOR FILING DATE: 1998-11-16
PRIOR APPLICATION NUMBER: 09/193,043
PRIOR APPLICATION NUMBER: 09/362,652
PRIOR FILING DATE: 1994-12-21
PRIOR FILING DATE: 1994-12-21
PRIOR FILING DATE: 1994-10-03
NUMBER OF SEQ ID NOS: 114
                                                                                                                                                       SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2
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US-09-891-943-2
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674 FDLALDPGRLTSRAIFNETKNPTLTRRKTLGLGIHCETLKLLLPDCVEDVVSPIILHLNF
                                  SLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVG
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Search completed: November 9, 2004, 12:46:58 Job time: 102.5 secs

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APPLICANT: Gallatin, W. Michael
APPLICANT: Van Der Vieren, Monica
TITLE OF INVENTION: No. 5437958el Human 2 Integrin Alpha
TITLE OF INVENTION: Subunit
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 233 S. Wacker Drive, 6300 Sears Tower Indels SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/173,497 FILING DATE: US-08-485-618-2 US-08-362-652-2 US-08-482-293A-2 US-08-943-363-2 US-09-193-043-2 US-09-193-043-2 US-09-150-259-2 US-08-560-618-99 US-08-665-618-99 US-08-665-618-99 US-08-482-293A-99 US-08-943-363-99 US-09-193-043-99 US-09-193-043-55 US-09-350-259-95 Score 5862; DB Pred. No. 0; 7; Mismatches ALIGNMENTS COUNIA...
ZIP: 60666-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
AMBUTHER: IBM PC compatible
"""TEM: PC-DOS/MS-DOS RESULT 1
US-08-173-497-3
Sequence 3, Application US/08173497
Patent No. 5437958
GENERAL INFORMATION: TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 1153 amino acids 99.8**%**; 99.3**%**; Best Local Similarity 99.3 Matches 1129; Conservative MOLECULE TYPE: protein single ADDRED: 235 STREET: 235 CITY: Chicago TYPE: amino acid STRANDEDNESS: sir linear 

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RINGTVIMDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDIP 1020
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            PPEALRGCPQEDSDIAFLVDGSGSIIPHDFRRAKEFISTVMEQLKKSKTLFSLMQYSBEF
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                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,889
                                                               APPLICANT: Gallatin, W. Mich
APPLICANT: Gallatin, W. Mich
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5470953el Human 2 Integr
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray
STREET: 233 South Wacker Drive, 6300 Sear Tower
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                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: P38,659
REFERENCE/DOCKET NUMBER: 27866/32168
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIPRICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
ATTORING AGENT INFORMATION:
NAME: Williams JT., JOSEPH A.
                                                                                                                                                                                                                                                                 COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                         US/08286889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.88;
                                                                                                                                                              STREET: 233 South Wacker D
CITY: Chicago
STATE: 111inois
COUNTRY: United States
ZIP: 6066-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1153 amino acids
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312-474-0448
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Best Local Similarity 99.3
Matches 1129; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                         Sequence 3, Application Patent No. 5470953 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: si
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RESULT 2
US-08-286-889-3
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         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
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99.3%; Pred. No. 0;
iive 7; Mismatches
                                           AFLILATION NUMBER: US/US/465,010
FILING DATE: CLASSIFICATION: 435
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1994
RPICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr.; Joseph A.
REGISTRATION NUMBER: 38,652
BREGISTRATION NUMBER: 38,652
BREGISTRATION NUMBER: 38,652
BREGISTRATION NUMBER: 38,652
BREGISTRATION NUMBER: 38,652
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 PC-DOS/MS-DOS
                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                     LENGTH: 1153 amino acids
                                                                                                                                                                                                                                                                                             TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                     amino acid
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Best Local Similarity
Matches 1129; Conserv
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US-08-485-618-3
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             QNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPL
                                                                    PRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLF
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cker Drive, 6300 Sear Tower
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Fatent No. 5728533
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5728533el Human
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Chicago
STATE: 111inois
COUNTRY: United States
ZIP: 6060-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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STREET: 233 South Wa
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US-08-485-618-3
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240 256 316 360 376 420 436 540

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27866/32391
38,659
         REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                        TELEFAX: 312-474-0448
TELEX: 25-3856
INPORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids
                                                                                                            STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
REGISTRATION NUMBER:
                                                                                                    amino acid
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US-08-362-652-3
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  YDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNF
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STREET: 233 South Wacker Drive, 6300 Sear Tower
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/08362652
Patent No. 5766850
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5766850el Human
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
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CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION WHERE: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STATE: Illinois
COUNTRY: United States
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                        0;
Length 1153;
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  Query Match
99.8%; Score 5862; D
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1129; Conservative 7; Mismatches
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233 South Wacker Drive, 6300 Sear Tower
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY AGENT INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5817515e1
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APPLICATION NUMBER: US/08/605,672
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Patent No. 5817515
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COUNTRY: United States
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INFORMATION FOR SEQ ID NO:
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
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TELEFAX: 3
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US-08-605-672-3
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       Length 1153;
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    Score 5862;
Pred. No. 0;
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Best Local Similarity 99.3
Matches 1129; Conservative
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                                                           TDGEKFGDPLGYEDVIPEADREGVIRYVIGYGDAFRSEKSRQELNTVASKPPRDHVFQIN
                                                                                                                  NFEALKTIQNQLREKI PAIEGTQTGSSSSFEHEMSQEGFSAAITSNGPLLSTVGSYDWAG
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US-08-943-363-3
; Sequence 3, Application US/08943363
; Patent No. 5837478
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           FFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLFGQGAFVRSQTET 1080
                           1037 FFGIQEEFNATIKGNLSFDWYIKTSHNHLLIVSTARILFNDSVFTLLPGQGAFVRSQTET 1096
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                                                                   KVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMMSEGGPPGAEPQ 1137
                                                                                  1097 KVEPFEVPNPLPLIVGSSVGGLILIALITAALXKLGFFKRQYKDMMSEGGPPGABPO 1153
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,293A
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                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5831029el Human
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27866/32684
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY,AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
REPERENCE/DOCKET NUMBER: 2786f
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
                                                                                                                                                                 Sequence 3, Application US/08482293A Patent No. 5831029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 312-4...
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
...VOTH: 1153 amino acids
                                                                                                                                                                                                                                                                                                        CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
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linear
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STREET: 250
Truv, Chicago
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TOPOLOGY: lin
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Matches 1129;
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US-08-482-293A-3
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RINGTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDIP 1020
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CURRENT FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: 08/173,497
EARLIER FILING DATE: 1993-12-23
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER FILING DATE: 1994-08-05
EARLIER PELING DATE: 1994-12-21
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1997-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/09193043
Patent No. 6251395
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 625139591
FILE REPERENCE: 27866/35004
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US-09-193-043-3
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233 South Wacker Drive, 6300 Sear Tower
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                                                                  ADDRESS...
ADDRESS...
STREET: 23.
STREET: 111inois
STATE: 111inois
STATE: United States
COUNTRY: United States
COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC Compatible
PERATING SYSTEM: PC-DOS/MS-DOS
"PE: Patentin Release #1.0, Version #1.25
"ATION DATA:
"PR: US/08/943,363
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APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5837478el Human
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION NOMBER: US/U8/943,363
FILING DATE:
CLASSIFICATION 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/103,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/266,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION UNMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams JT., JOSEPPA.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 236,659
REFERENCE/DOCKET NUMBER: 236,659
REFERENCE/DOCKET NUMBER: 236,659
REFERENCE/DOCKET NUMBER: 27866/32684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPAONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids
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MOLECULE TYPE: protein
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FILE REFERENCE: 27866/36646
CURRENT APLICATION NUMBER: US/09/688,307A
CURRENT FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 08/13,497
PRIOR APPLICATION NUMBER: 08/13,497
PRIOR APPLICATION NUMBER: 08/13,497
PRIOR FILING DATE: 1994-02-22
PRIOR FILING DATE: 1994-02-23
PRIOR FILING DATE: 1994-05-652
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PRIOR FILING DATE: 1994-05-652
PRIOR FILING DATE: 1994-05-652
PRIOR FILING DATE: 1994-06-05
PRIOR FILING DATE: 1994-08-05
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PRIOR FILING DATE: 1994-08-05
PRIOR FILING DATE: 1994-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PATENT VALUE APPLICATION NUMBER: 08/943,363
PRIOR FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
                                                                                                                                                                                                                                          Sequence 3, Application US/09688307A Patent No. 6432404 GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
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Matches 1129; Conservative
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Pred. No. 0;
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                NUMBER OF SEQ ID NOS: 11 SOFTWARE: Patentin Ver. SEQ ID NO 3
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7; Mismatches
                        943,363
       EARLIER FILING DATE: 1994-12-21
EARLIER APPLICATION NUMBER: 08/943;
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 3
LENGTH: 1153
TYPE: PRT
TYPE: PRT
TO CREATENT HOME SAPIENS
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Best Local Similarity
Matches 1129; Conserv
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US-09-350-259-3
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                     GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR
                                   PRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLF
                                                                  QNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPL
                                                                               HGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTWDGLVDLTVGAQGHVLLLRSQ
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Patent No. 6620915
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVERTION: No. 6620915el Human 2
FILE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/350,259
CURRENT FILING DATE: 1999-07-08
EARLIER APPLICATION NUMBER: 09/193,043
EARLIER FILING DATE: 1998-11-16
EARLIER FILING DATE: 1993-12-23
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-08-05
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                                                  GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR
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                                                                        QNTGMWESNANVKGTQ1GAYFGASLCSVDVDSNGSTDLVL1GAPHYYEQTRGGQVSVCPL
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APPLICANT: ARNAOUT, M. AMIN

TITLE OF INVENTION: HUMAN CR3a/b HETERODIMERS

TURENT APPLICATION HUMBER: 12

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/78,871

FILING DATE: 16-JUN-1993

PRIOR APPLICATION NUMBER: 539,842

FILING DATE: 18-JUN-1990

APPLICATION NUMBER: 212,573

FILING DATE: 28-JUN-1988
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                                                                                                                             Sequence 43, Application PC/TUS9601314
GENERAL INFORMATION:
APPLICANT: M. Amin Arnaout
TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN
TITLE OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                            COUNTER TO SA A SACRAGUE OF TABLE OF THE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABL
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99.0%; Pred. No. 0;
ive 7; Mismatches
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ER: 00786/267001
                                                                                                                                                                                                                                                                              ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: John W. Freeman
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 0078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                           PCT-US96-01314-43
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PCT-US96-01314-43
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APPLICATION NUMBER: US/08/476,062A FILING DATE: 07-7UN 1995
PRIOR APPLICATION DATA: 1994
APPLICATION NUMBER: 08/216,081
FILING DATE: 21-MAR 1994
APPLICATION NUMBER: 07/637,830
FILING DATE: 04-7AN 1991
APPLICATION NUMBER: 07/539,842
FILING DATE: 18-7UN 1990
APPLICATION NUMBER: 07/212,573
FILING DATE: 18-7UN-1986
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W. REGISTATION NUMBER: 29,066
                                                                    RESULT 14
US-08-476-062A-44
Sequence 44, Application US/08476062A
Patent No. 5877275
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 61.0%; Pr
Matches 689; Conservative 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 00:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1163 amino acids
                                                                                                                                                                                                                                                                          IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                   ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
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TITLE OF INVENTION: CONTROLLING CELLULAR IMMUNE/INFLAMMATORY
TITLE OF INVENTION: RESPONSES WITH BETA2 INTEGRINS
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Richardson P.C.
STREET: 225 Franklin Street Indels 59.0%; Score 3469; DB 2; 61.0%; Pred. No. 7e-284; tive 141; Mismatches 293; FastSEQ for Windows Version 2.0

Richardson P.C. Street

225 Franklin

Fish &

ADDRESSEE:

CITY: Boston STATE: Massachusetts

COUNTRY:

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: Ms-DOS (Version 5.0)
CURRENY APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/01314
FILING DATE: 30-JAN-96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/380,167
FILING DATE: 30-JAN-95
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 29,066
RESPERBURGE/DOCKET NUMBER: 29,066
RESPERBURGE/DOCKET NUMBER: 29,066
RESPERBURGE/DOCKET NUMBER: 29,066
RESPERBURGE/DOCKET NUMBER: 29,066
RESPERBURGE/DOCKET NUMBER: 29,066
RESPERBURGE/DOCKET NUMBER: 29,066
REBERBURGE/DOCKET NUMBER: 29,066
REBERBURGE/DOCKET NUMBER: 29,066
REBERBURGE/DOCKET NUMBER: 20-2000
TELEPRAN: 20015A
RELEPRAN: 20015A

TELEX: 200154 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS LENGTH: 1163

amino acid

; TOPOLOGY: linear PCT-US96-01314-44 STRANDEDNESS:

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360
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       Length 1163;
Query Match 59.0%; Score 3469; DB 5; Length 1 Best Local Similarity 61.0%; Pred. No. 7e-284; Matches 689; Conservative 141; Mismatches 293; Indels
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APPLICANT: M. Amin Arnaout
TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN
TITLE OF INVENTION: ANTAGONISTS
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:

Sequence 44, Application PC/TUS9601314 GENERAL INFORMATION:

PCT-US96-01314-44

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960 VRINQTVIWDRPQVIFSENLSSTCHIKERLPSHSDFLAELRKAPVVNCSIAVCORIQCDI 1019
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Search completed: November 9, 2004, 12:21:09 Job time: 28 secs

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Compugen Ltd.
 GenCore version
Copyright (c) 1993 - 2004
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using sw model protein search, OM protein

Run on:

November

9, 2004, 11:57:37; Search time 27.25 Seconds (without alignments) 4014.622 Million cell updates/sec

US-09-902-481B-6

Title: Perfect score:

5875 1 FNLDTENAMTFQENARGFGQ......FKRQYKDNMSEGGPPGAEPQ 1137 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

residues 96216763 283416 seqs, Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 DB DB Minimum

Maximum

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 79:\* Database

pir1:\* pir2:\* pir3:\* 1 2 E 4 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|    |        | d                   |        |    | SUMMARIES |                    |
|----|--------|---------------------|--------|----|-----------|--------------------|
|    | Score  | %<br>Query<br>Match | Length | DB | CI        | Description        |
| 1  | 5868   | 99.66               | 1153   | -  | RWHU1B    | cell surface glyco |
| 7  | 4476   | •                   | 1153   | 7  | 800551    | eukocvte surface   |
| m  | 3483   | 5                   | 1163   | Н  | RWHU1C    | ace                |
| 4  | 1548.5 | 7                   | 1170   | N  | 803308    | surfac             |
| S  | 1533.5 | 26                  | 1163   | 0  | 156126    | hocyte fu          |
| 9  | 1149   | 7                   | 1179   | ~  | A53213    | al                 |
| 7  | 1102.5 | 18.                 | 1151   | 0  | A45226    | alpha-1            |
| 60 | 1084   | 7                   | 1170   | 7  | I45914    | alpha 2            |
| σ  | 1072   | 18.                 | 1178   | ~  | S44142    | otein hom          |
| 10 | 1069   | 18.                 | 1181   | 7  | A33998    | н                  |
| 11 | 1060   | 7                   | 1180   | 7  | A35854    | alpha-             |
| 12 | 663    | П                   | 1039   | ~  | A41131    |                    |
| 13 | 633    | 10.                 | 1038   | ~  | S06046    | alpha-4            |
| 14 | 630    | Н                   | 1035   | 7  | I58409    |                    |
| 15 | 614.5  | 10.                 | 1041   | ~  | T31437    | 디                  |
| 16 | 579.5  |                     | 1054   | N  | JC7294    | nteg               |
| 17 | 572.5  | ο,                  | 1051   | ~  | A35761    |                    |
| 18 | 567.5  | 9.                  | 1053   | 7  | I55534    | VLA-3 alpha subuni |
| 49 | 555.5  | 9.                  | 1053   | 7  | S44250    | integrin alpha-5 c |
| 20 | 543.5  | 9.3                 | 1034   | 7  | A3610B    | alpha-V            |
| 21 | 535    |                     | 1044   | 7  | T10050    | integrin alpha-v c |
| 22 | 532    |                     | 1049   | 7  | A27079    | tin recep          |
| 23 | 532    |                     | 1073   | 7  | B36429    | integrin alpha-6 c |
| 24 | •      | 9.0                 | 1072   | 7  | A38457    | alpha-6            |
| 25 | 529.5  |                     | 1051   | ~  | A40021    | alpha-3            |
| 26 | 52     | 9.0                 | 1048   | 7  | A27421    |                    |
| 27 | 525.5  |                     | 1091   | 7  | A41543    |                    |
| 28 | 21     |                     | 1044   | ~  | 816516    | alpha-8            |
| 29 | 496.5  | 8.5                 | 1146   | ~1 | \$40311   | integrin - fruit f |

| integrin alpha-2b | position-specific | integrin alpha-7 c | alpha-7 integrin - | leukocyte adhesion | glycoprotein IIb - | integrin alpha cha | F54F2.1 protein - | integrin alpha v c | hypothetical prote | integrin alpha cha | integrin alpha cha | glycoprotein IIb - | integrin alpha cha | qlycoprotein IIb - | integrin alpha-1 - |
|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| 69                | 637               | 950                | 186                | B30892             | 0163               | 8783               | S44824            | 0571               | 8277               | 19403              | r09433             | 6916               | .8523              | 6917               | 155348             |
| A34269            | A29               | JCS                | 161                | B3                 | A6                 | 83                 | S                 | S6                 | S                  | Ë                  | Ĕ                  | 13                 | H                  | 13                 | A                  |
| 2 A342            | 2 A29             | 2 JC5              | 2 I61              | 2 B3               | 2 A6               | 2 83               | 2 S4              | 2 S6               | 2 \$2              | 2 IC               | 7                  | 2 I3               | 2 T1               | 2 I3               | 2 A5               |
| 2                 | 1394 2 A29        | 7                  | 8                  | 7                  | 7                  | ~1                 | C)                | 7                  | 0                  | 21                 | N                  | ~                  | 21                 | ~                  | 7                  |
| 1039 2 A          | 7                 | 1137 2             | 1135 2             | 126 2              | 1037 2             | 1106 2             | 1226 2            | 1045 2             | 1139 2             | 1115 2             | 1115 2             | 764 2              | 1086 2             | 604 2              | 272 2 1            |
| 8.4 1039 2 A      | 1394 2            | 8.3 1137 2         | 8.3 1135 2         | 8.3 126 2          | 8.3 1037 2         | 1106 2             | 7.9 1226 2        | 7.7 1045 2         | 7.6 1139 2         | 7.2 1115 2         | 7.1 1115 2         | 6.7 764 2          | 5.3 1086 2         | 5.1 604 2          | 5.0 272 2 1        |

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cell surface glycoprotein CD11b precursor [validated] - human N'Alternate names: complement receptor type 3 alpha chain; leukocyte adhesion protein Me eukocyte integrin alpha chain; neutrophil adherence receptor alpham chain

IJ C;Species: Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence revision 31-Dec-1992 #text\_change 09-Jul-2004
C;Date: 31-Dec-1992 #sequence revision 31-Dec-1992 #text\_change 09-Jul-2004
C;Accession: A31108; A28915; A41600; A30892; A32218; A46526; A26091; I52567
R;Corbi, A.L.; Kishimoto, T.K.; Miller, L.J.; Springer, T.A.
J. Biol. Chem. 263, 12403-12411, 1988
A;Title: The human leukocyte adhesion glycoprotein Mac-1 (complement receptor type 3,

A.Reference number: A31108; MUID:88315033; PMID:2457584
A;Accession: A31108
A;Accession: A31108
A;Accession: A31108
A;Accession: A31108
A;Accession: A31108
A;CRS-references: UNIPROT:P11215; GB:J03925; NID:g187284; PIDN:AAA59544.1; PID:g307148
A;Note: part of this sequence was confirmed by protein sequencing
B;Arnaout, M.A.; Gupta, S.K.; Prerce, M.W.; Tenen, D.G.
Cell Biol. 106, 2153-2158, 1988
A;Title: Amino acid sequence of the alpha subunit of human leukocyte adhesion receptor NA;Reference number: A28915; MUID:88257215; PMID:2454931

A.Accession: A28915
A.Molecule type: MRNA
A.Rossion: A28915
A.Molecule type: MRNA
A.Rossion: A28915
A.Molecule type: MRNA
A.Rosidues: 1-499, 501-1055, 'P', 967-1153 cARN>
A.Rosidues: 1-499, 501-965, 'P', 967-1153 cARN>
A.Rosidues: 1-499, 501-965, 'P', 967-1153 cARN>
A.Note: part of this sequence, including the amino end of the mature protein, was confin R.Shelley, C.S.; Arnaout, M.A.
Broc. Natl. Acad. Sci. U.S.A. 88, 10525-10529, 1991
A.Title: The promoter of the CD11b gene directs myeloid specific and developmentally reg A.Rocession: A41600
A.Molecule type: DNA
A.Rosidues: 1-9 cSHE>
A.Rosidues: 1-9 cSHE>
A.Rosidues: 1-9 cSHE>
A.Cross-references: GB:M76724; NID:g180018; PIDN:AAA58410.1; PID:g553215
R.Arnaout, M.A.; Remold-O-Donnell, B.; Pierce, M.W.; Harris, P.; Tenen, D.G.
Proc. Natl. Acad. Sci. U.S.A. 85, 2776-2780, 1988
A.Title: Molecular cloning of the alpha-subunit of human and guinea pig leukocyte adhes:
A.Rosicular cloning of the alpha-subunit of human and guinea pig leukocyte adhes:
A.Rosicular cloning of the alpha-subunit of human and guinea pig leukocyte adhes:

A, Accession: A30892 A, Molecule type: mRNA A, Residues: 917-1042 <AR2>

A,Cross-references: GB:M18044
R;Hickstein, D.D.; Hickey, M.J.; Ozols, J.; Baker, D.M.; Back, A.L.; Roth, G.J.
R;Hickstein, D.D.; Hickey, M.J.; Ozols, J.; Baker, D.M.; Back, A.L.; Roth, G.J.
Rroc. Natl. Acad. Sci. U.S.A. 86, 257-261, 1989
A;Title: CDNA sequence for the alphaM subunit of the human neutrophil adherence recepton A;Reference number: A32218; MUID:89098993; PMID:2563162

A;Molecule type: mRNA A;Residues: 9-1153 <HIC> A;Cross-references: GB:J04145; NID:g189068; PIDN:AAA59903.1; PID:g386975

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Teukocyte surface glycoprotein Mac-1 alpha chain precursor - mouse
Nighternate names: complement-3 receptor alpha chain
Signates: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1899 #sequence revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: S00551; 159078
R;Pytela. R.
R;Pytela. R.
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R;Pytela. R.
R;Pytela. Mulo acid sequence of the murine Mac-1 alpha chain reveals homology with the A;Title: Amino acid sequence of the murine Mac-1 alpha chain reveals homology with the A;Title: Amino acid sequence of the murine Mac-1 alpha chain reveals homology with the A;Title: Amino acid sequence of the murine Mac-1 alpha chain reveals homology with the A;Title: Amino acid sequence of the murine Mac-1 alpha chain reveals homology with the A;Molecule type: DNA
A;Residues: 1-1133 cPyT-
A;Residues: 1-1133 cPyT-
A;Residues: 1-1133 cPyT-
A;Cross-references: UNIPROT:PODS555; EMBL:X07640; NID:952982; PIDN:CAA30479.1; PID:95298
A;Note: the authors translated the codon CAC for residue 569 as Gln
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NFEALKTIQNQLREKIFALEGTQTGSSSSFEHEMSQEGFSAAITSNGPLLSTVGSYDWAG
                                                                                                                                                                                                                                 PRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLF
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                                                                                                    GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR
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                                                                  A; Title: Structural analysis of the CD11b gene and phylogenetic analysis of the alpha-ir during evolution.

A; Reference number: A46526; MUID:93123748; PMID:8419480

A; Accession: A46526; MUID:93123748; PMID:8419480

A; Accession: A46526; MUID:93123748; PMID:8419480

A; Accession: A46526

A; Status: not compared with conceptual translation

A; Molecule type: DNA

A; Reciences: Capacity of the CD11b are included in some but not all mature A; Note: the last three bases of intron 13, CAG, are included in some but not all mature A; Note: sequence extracted from NEBI backbone (NCBIP:121963)

A; Note: sequence extracted from NEBI backbone (NCBIP:121963)

B; Note: sequence extracted from NEBI backbone (NCBIP:121963)

R; Peterce, M. W.; Remold-O'Donnell, E.; Todd III, R.F.; Arnaout, M.A.

Biochim. Biophys. Acta 874, 368-371, 1986

A; Title: N. terminal sequence of human leukocyte glycoprotein Mol: conservation across spansoluse: 17-31 cpie.

A; Molecule type: protein

A; Molecule type: protein

A; Molecule type: protein

A; Residues: 17-31 cpie.

A; Residues: 17-31 cpie.

A; Residues: 17-31 cpie.

A; Residues: 17-31 cpie.

A; Residues: 17-31 cpie.

A; Residues: 15-367; MUID:92144986; PMID:1346576

A; Reference number: 152567; MUID:92144986; PMID:1346576
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A;Cross-references: GDB:120599; OMIN:120980
A;Gene: GDB:ITGAM; CR3A
A;Cross-references: GDB:120599; OMIN:120980
A;Amap position: 16p11.2-16p11.2
A;Nate: promoter contains a GATA motif and two Sp1 consensus binding sites
C;Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat home
C;Keywords: alternative splicing; calcium; cell adhesion; glycoprotein; heterodimer; mag
F;1-16/Domain: signal sequence #status predicted cSIG>
F;1-1108/Domain: extracellular #status predicted cEXT>
F;148-318/Domain: calcium/magnesium binding #status predicted
F;530-538/Region: calcium/magnesium binding #status predicted
F;530-538/Region: calcium/magnesium binding #status predicted
F;530-61/Region: calcium/magnesium binding #status predicted
F;1109-1134/Domain: transmembrane #status predicted cINT>
F;146.240,391,469,693,697,735,802,881,901,912,941,947,979,994,1022,1045,1051,1076/Binding
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     was confirmed by protein sequencing
Gonzalez, D.A.; Smith, T.F.; Tenen, D.G.
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     A;Note: part of this sequence was R;Fleming, J.C.; Pahl, H.L.; Gonza J. Immunol. 150, 480-490, 1993
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R;Sastre, L.; Roman, J.M.; Teplow, D.B.; Dreyer, W.J.; Gee, C.E.; Larson, R.S.; P. Porco, Natl. Acad. Sci. U.S.A. 83, 5644-5648, 1986
A.Title: A partial genomic DNA clone for the alpha subunit of the mouse complement A;Reference number: 159078, MUID:86287312; PMID:2942940
A;Accession: 159078
A;Status: preliminary; translated from GB/EMBL/DDBJ
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1020 PFFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLPGQGAFVRSQTE
                                      Query Match 26.4%; Score 1548.5; DB 2; Dength 11.00; Best Local Similarity 34.5%; Pred. No. 4.38-98; Matches 405; Conservative 208; Mismatches 460; Indels 101; Gaps
                                                                                                                                                          Length 1170;
                                                                                                                             TKVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKROYKDMMSE
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                                     310 FVKILDTFEKLKDLFTELQKKIYVIEGTSKQDLTSFNMELSSSGISADLSRGHAVVGAVG
                                                                                                                                                                                 AKDWAGGELDLKADLQDDTFIGNEPLTPEVRAGYLGYTVTWLPSRQKTSLLASGAPRYQH
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                                                                     KILIVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRD
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J. Immunol. 147, 369-374, 1991
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J. Immunol. 147, 369-374, 1991
J. Immunol. 147, 369-374, 1991
J. Immunol. 147, 369-374, 1991
J. Islandor of the murine lymphocyte function-associated molecule-1 alpha-subunit A, Reference number: I56126, MUID:91268576; PMID:2051027
A, Accession: I56126
A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Residues: 1-1163 - RES-
A, Cross-references: UNIPROT:P24063; GB:M60778; NID:g198785; PIDN:AAA39426.1; PID:g19878
A, Cross-references: UNIPROT:P24063; GB:M60778; NID:g198785; Conetic IRA-1
C, Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat hom F;151-315/Domain: von Willebrand factor type A repeat hom
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Amphocyte fuction-associated molecule-1-alpha
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| DD 295 SSHGSRRKASKVMVVLTDGGIFEDPLNLTTVINSPKMQGVERFAIGVGEEFKSARTAREL 354 | Qy 285 NIIASKPPRDHVFQVNNFEALKTIQNQLREKIPAIEGTQTGSSSSFEHEMSQEGFSAAIT 344 | MALDGLLSKLRYNIISMEGTVGDALH   | 345 SNGP-LLSTVGSYDWAGGVELY-TSKEKSTPINMTRVDSDMNDAYLGYAAAIILEN | 412 DERQVLLGAVGAFDWSGGALLYDTRSRRGRFLNQTAAAADAEAAQYSYLGYAVAVLHKT             | OY 399 RVOSLVUGARPYCHICLVAMPR-ONTCHWESNAN'S ACTOICARYEABLE/SVOVDISMOST 456  10  | Qy 457 DLVLIGAPHYYEQTRGGQVSVCPLPRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVN 516 | 530 DFLLIVAAPPYHVHGEEGRVYVYRLSE-QDGSFSLARILSGHPGFTNARFGFAMAAMGDLS     | Qy 517 GDKLTDVALGAPGEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGQ 570<br> | Qy 571 SLSGGQDLTMDGLVDLTVGAQGHVLLLRSQPVLRVKAIMERNPREVARNVFECNDQVVKG 630 | 648 SERGGEDESCUGLANDILVGILGGANVERSKEVVELKUSFGAFETESALE<br>631 KEAGEVRVCLHVQKSTRDRLEGGIQSVVTYDLALDSGRPHSRAVFNBTKNSTRRQTQVL<br>    : | Db 698 NGVVNVŘLČFEI-SSVTTASESGIREALINFTĽDVDVGKQRRŘLQCSDVRSCLGCLREWS 756 | QY 691 GLTQTCETLKLQLPNCIEDPVSPIVLRINFSLVGTPLSAFGNIRPVLAEDAQRLFT 746 : | QY 747 ALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVGGPREFNVTVTVRNDGEDSYRTQVTFF 806   | QY 807 PPLDLSYRKVSTLQNQRSQRSWRLACESASSTEVSGALKSTSCSINHPIFPENSEVTFNI 866 | CASLG<br> <br>IAFPN | QY 920 STKYINFTASENTSRVMQHQYQVSNLGQRSLPISLVFLVFVRLNQTVIWDRPQVTFSE 977 | QY 978 NLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDIPFFGIQEEFNATLKGNLS 1037 ::   ::   | QY 1038 FDWYIKTSHNHILIVSTAEILENDSVFTLLPQQGAFVRSQTETKVEPFEVPNPL 1091  | Qy 1092 PLIVGSSVGGLLIALITAALYKLGFFKRQYKDMMSE 1128<br> : :        :                Db 1126 PIIIKGSVGGLLVLIVILFKCGFFKRKYQQLNLE 1162 | RESULT 7<br>A45226<br>integrin alpha-1 chain - human (fragment)   | C;species: Home Sapiens (man)<br>C;Daces: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004<br>C;Accession: A45226<br>R;Briesewitz, R.; Epstein, M.R.; Marcantonio, B.E.<br>J. Biol. Chem. 268, 2989-2996, 1993<br>A;Tiile: Expression of native and truncated forms of the human integrin alpha 1 subunit |
|---|---|--|--|---|---|---|---|---|---|--|---|---|---|---|---------------------|---|--|--|---|---|--|
| <br>   <br>   | Db 775 ANLTLSSPARSGPLRLMSSASLAVEWTLSNSGEDAYWVRLDLDFPRGLSFRKV 827        | QY 817 STLONQRSQRSWRLACESASSTEVSGAL-KSTSCSINHPIPPENSEVTFNITFDVDSKAS 875 DE | EMLQPHSRMPVSCBELTEGSSLLTKTLKCNVSSPIFKAGQEVSLQVMFNTLLNSS 882  | 876 LGNKLLLKANVTSEN-NMPRTNKTEPQLELPVKYAVYMVVTSHGVSTKYLNFTASENTSR 934<br>: : | Db 883 WEDFVELNGTVHCENENSSLQEDNSAATHIPVLYPVNILTKEQENSTLYISFTFKGPKTQ 942 Qy Qy 935 VMQHQYQVSNLGQRSLPISLVFLVPVRLNQTVIWDRPQVTFSENLSSTCHTK 986 DE | Db 943 QVQHVYQVRIQPSAXDHNMPT-LEALVGVPRPHSEDLITYTWSVQTDPLVTCHSE 996 Q3   | 987 E-RLPSHSDFLAELRKAPVVNCSIAVCQRIQCDIPFFGIQEEFNATLKGNLSFDWYIKTS 1045 | 1042  | 1043 -STLSLCSSLSVSFNSSKHFHLYGSKA-SEAQVLVKVDLIHEKEMLHVYVLSGIGGLVLL 1100  | DD 1101 FLIFLALYKVGFFKRNLKEKMEADGGVPRGSP 1132  |   |   | C;Date: 19-Oct-1995 #sequence_revision 31-Mar-2001 #text_change 09-Jul-2004 C;Accession: A53213 R;Shaw, S.K.; Cepek, K.L.; Murphy, E.A.; Russell, G.J.; Brenner, M.B.; Parker, C.M. J. Biol. Chem. 269, 6016-6025, 1994 D | subunit. Un   |                     | r type A repeat homd  | on Willebrand factor type A repeat homology <vwa3> 19.6%; Score 1149; DB 2; Length 1179; rity 29.1%; Pred. No. 1.5e-70;</vwa3> | #ACCHES 343; CONSEIVATIVE ZII; MISMACCHES 431; INDELS 1/2; Gaps 35; 45 GSLYQCDYSTGSCEPI-RLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQ 95 | DD  | QY         120 KFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQL 164         R1           Db         175 RQRRALEKEEEBDKEEBEBEEBEAGTEIAIILDGSGSIDPPDFQRAKDFISNMRNFYE 234         1.1 | OY 165 KKSKTLFSLMQYSEEFRIHFTFKEFQNNPNPRSLVKPITQLIGRTHTATGVRKVIRELLN 224    :   :   :   :   :   :     :   |

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A,Status: preliminary; not compared with conceptual translation A,Status: preliminary; not compared with conceptual translation A,Status: 1-1151 - 8R1.
A,Residues: 1-1151 - 8R1.
A,Experimental source: hopatoblastoma cell line HepG2
A,Experimental source: hepatoblastoma cell line HepG2
A,Note: sequence extracted from NCB1 backbone (NCBIP:124326)
F;142-317/Domain: von Willebrand factor type A repeat homology <
                                                                                                                                                          Length
                                                                                                                                                     Query Match
18.8%; Score 1102.5; DB 2; Length
Best Local Similarity 27.8%; Pred. No. 2.4e-67;
Matches 344; Conservative 211; Mismatches 487; Indels
A; Reference number: A45226; MUID:93155124; PMID:8428973
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KSTSCSINHPIFPENSEVTFNITFDVDSKASLGN-KLLLKANVTSENNMPRTNKTEFQLE 903
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C.Species: Bos primigenius taurus (cattle)
C.Species: Bos primigenius taurus (cattle)
C.Daccession: 145914
A.Title: Identification of putative ligand binding sites within the I-domain cA.Reference number: A54402; MUID:94193647; PMID:7511592
A.Accession: 145914
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A.Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                          992 HSDFLAELRKAPVVNCSIAVCQRIQCDIPFFGIQE---
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A;Cross-references: UNIPROT:Q62469; EMBL:Z29987; NID:9473098; PIDN:CAA82877.1; PID:9473
F;169-344/Domain: von Willebrand factor type A repeat homology <VWA2>
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R;Edelman, J.M.; Chan, B.M.; Uniyal, S.; Onodera, H.; Wang, D.Z.; Damjanovich, L. Bibmited to the EMBL Data Library, January 1994
R;Edelman, J.M.; Chan, B.M.; Data Library, January 1994
R;Description: The mouse VLA-2 homologue supports collagen and laminin adhesion A;Reference number: S44142
A;Accession: S44142
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A;Accession: S44142
A;Accession: S44143
A;Residues: 1-1178 < EDE>
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C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                  RFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLFHGTSGSGISPSHSQRIAGS--KL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ECNDQVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVTYDLALD----SGRPHSRAVFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | | : : | | | : : | | | : | : | | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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905 928 955

-SLPISLV :

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| Db 929 LLYDARIHIA-RSTNINFYRTGSDRNABGVIKgyrdigdreifgi kymaggaddgn 600   | <del>-</del>                      |   |
|--|-----------------------------------|---|
| PVRLNOTVIWDRPOVTF-SENIS  | ob du                             | 90 ATCEKLNLQTSTSIPNVTEMKTNMSLGLILTRNMGTGGFLTCGPLWAQQCGNQYYTTGVC 149   |
| :  | 108                               | FRRMKEFVSTVMEQLK  |
| Qy 981 STCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDIPFFGIQEEFNATLKGNLSFDW 1040   | 150                               |   |
| Db 1041HTKB  | Oy 166 KSK                        | KSKTLFSIMQYSBEFRIHFTFKEFQNNFNPRSLVKPITQLIG-RIHTATGVRKVIRELLN 224  |
| QY 1041 YIKTSHNHLLIVSTAEILFNDSVFTLLPGQGAFVRSQTETKVEPFEVPNPLPLIVGSSVG 1100 ::::::::   | 225                               |   |
| Qy 1101 GLLLLALITAALYKLGFPKRQYKDM 1125<br> :    :    :   | 266                               |   |
| Db 1139 GILLLAMTAGLWKLGFFKRQYKKM 1163  |                                   | SKQELNIJASKFFKUHFQVNNFEALKIIQNQLKKKIFALBGIQIGSSSSFFHEMSQEGF 339<br>   |
|  | Qy 340 SAA<br>   <br>  Db 384 SAD | SAAITSNGPLLSTVGSYDWAGGVFLYTSKEKSTFINMTRVDSDMN-DAYLGYAAAI 394<br>   :  :     :  :     SADYSSQNDILMLGAVGAFGWGGTIVQKTSHGHLIFPRQAFDQILQDRNHSSYLGYSVAA 443 |
| N.Alternate names: CD49D; platelet glycoprotein GPIa; VLA-2/collagen receptor alpha-<br>C;Species: Homo sapiens (man)<br>C;Date: 30-Mar-1990 Hsequence revision 18-Sep-1992 #text_change 09-Jul-2004                               | 395                               |   |
|  | Oy 449                            | GESTHFVAGAFKANYTGQIVLYSVNENGNITVIQAHRGDQIGSYFGSVLCSV 498<br>SNGSTDLVLIGAPHYYEQTRGGQVSVCPLPRGQRARWQCDAVLYGEQGOPWGRFG 506                               |
| ;Title: The primary structure of the VLA-2/collagen receptor alpha(2)-subunit (plat;Reference number: A33998; MUID:89308879; PMID:2545729<br>- Ancression: A33998  | 499                               |   |
|  | QY - 507                          | AALTVLGDVNGDKLJDVAIGAPGEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPR 564  |
| ;Cross-references: UNIPROT:P17301; GB:X17033; NID:g33906; FIDN:CAA34894.1; PID:g33907; Southers translated the codon GAT for residue 802 as Gln, GTC for residue 803; Catimell, B.: Parmentier, S.: Tennor, T. T.: Angreone, J. T. | Db 556                            |   |
| iochem. J. 279, 419-425, 1991<br>1711e: Separation of important new platelet glycoproteins (GPIa, GPIc, GPIc*, GPII)   | 615                               | LOYFGRSLDGYGDLGGCDUTHUCHULLYGAQGTVLLKYAATMENFKEVAKNYFELN 024 LQYFGRSLDGYGDLHODSTTDVSIGAFGQVVQLMSQSIADVAIEASFTPEKITLVNKN 672                           |
| Ancersion: B16793<br>:Molecule type: protein   | Qy 625 DQV                        | DQVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVTYDLALDSGRPHSRAVFNETK 680  |
| ;Residues: 30-43 <cat><br/>;Experimental source: platelet</cat>  | Db 673 AQII                       | ILKLCFSAKFRPTKQNNQVAIVYNITLDADGFSSRVTSRGLFKENN 721  |
| , A.<br>of nositive and  | Qy 681 NSTI                       | NSTRROTOVLGLTQTCETLKLQLPNCIEDPVSPIVLRINFSLVGTPLSAFGNLRPVLA 738  |
|  | OV 739                            | FNVTVTVRND  |
| (<br>(   | 773                               |   |
| ).t.oss-terefices: os:ldatz1; ntD:g40034Z; rlDN:AMA16619.Z; rlD:g4583335<br>;Note authors translated the codon GTA for residue 17 as Leu<br>.Genetics:   | Qy 795 GED                        | GEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASST-EVSGALKSTSCSINH 853  |
| Gene: GDB:ITGA2; CD49B<br>.Cross-references: GDB:128031; OMIM:192974   | Db 833 RES                        | :   :   :   :   :   :   :     :     :     :     :     :       :       :       :       :   |
| Map position: 5q11.1-5q11.2<br>:Keywords: cell adhesion; qlycoprotein; heterodimer: transmembrane protein  | Qy 854 PIF                        | PIFPENSEVIFNITFDVDSKASLGNKLLLKANVISENNMPRTNKTEFQLELPVKYAVYMV 913  |
| ,  | Db 881 PALI                       | PALKREQQVIFTINFDFNLQ-NLQNQASLSFQALSESQEENKADNLVNLKIPLLYDAEI- 938  |
| :172-347/Domain: von Willebrand factor type A repeat homology <vwa2></vwa2>  | 914 V                             | VISHGVSTKYLNFTASENTSRVMQHQYQVSNLGQRSLPISLVFLV 958   |
| ;1155-1181/Domain: intracellular #status predicted <cyt><br/>;105,112,343,432,460,475,699,1057,1074,1081/Binding site: carbohydrate (Asn) (covalent)</cyt>   | - 626                             | HLTRSTNINFYEISSDGNVPSIVHSFEDVGPKFIFSLKVTTGSVÞVSMATVIIHIPQ 995   |
| ŧ  | 959 YQ                            | **************************************  |
| Macches 331; Conservative 212; Mismacches 494; indels 188; Gaps  | Qy 989 LPS!                       | LPSHSDFLAELRKAPVVNCSIAVCQRIQCDIPFFGIQEEFNATLKGNLSFDWYIKTSHNH 1048   |
| OY I FULDIEMANTE C-ENARCH GOS VOLC   | Db 1048                           |   |
|  | Qy 1049 LLI                       | LLIVSTAEI-LFNDSVFTLLPGGGAFVRSQTETKVEPFEVPNPLPLIVGSSVG 1100  |

| Qy 617 ARNVFECNDQVXKGKEAGEVRVCLHVQ-KSTRDRLREGQIQSVVTYDLALDSGREHSR 673  Db 681 NIQKKNCRVEGKETVCINATMCFHVKLKSKEDSIYEADLQYRVTLDSLRQISR 733  Qy 674 AVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRL 718  Oy 674 AVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRL 718  OA 674 AVFNET | 719 NFSLVGTPLSAFGNLRPVLAEDAQRIFTALFPFERNCGNDNICQDDLSITFSFMSLDCLV 719 NFSLVGTPLSAFGNLRPVLAEDAQRIFTALFPFERNCGNNICQDDLSITFSFMSLDCLV 717 DFNLT_DFNGGPVLDDALPNSVHEHIPFARCGNKER[   | RESULT 12  1/44131  1 |
|--|--|--|
| Db 1092 VQLTAAABINTYNPBIYVIBDNTVTIPLMIMKPDBKAEVPTGVIIGSIIA 1141 Qy 1101 GLLLALITAALYKLGFFKRQYKDM 1125  | RESULT 11 integrin alpha-1 chain precursor - rat C;Species: Rattus morvegicus (Norway rat) C;Date: 23-0ct-1990 #sequence_revision 13-Sep-1991 #text_change 09-Jul-2004 C;Accession: A35864; S11243 C;Accession: A35864; S11243 C;Call Biol. 111, 709-720, 1990 A;Title: Molecular cloning of the rat integrin alpha-1-subunit: a receptor for laminin a A;Reference number. A35864; MUID: 90338125; PMID: 2380249 A;Reference number: A35864; MUID: 90338125; PMID: 2380249 A;Reference number: A35864; MUID: 90338125; PMID: 2380249 A;Reference: JNIBO clON> A;Reference: JNIBO clON> A;Residues: 1-1180 clON> A;Residues: JNIBO cloN> A;Residues: JNIBO cloN> A;Residues: JNIBO cloN> A;Residues: JNIBO cloN> A;Residues: JNIBO cloN> A;Residues: J | OY 166 -KSKTLFSLMQYSEEFRIHFTEKEPONNPNPRSLVKPITQLLG-RTHTATGVRKVIRELL 223  1   |

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989 LPSHSDFLAELRKA-----PVVNCSIAVCQRIQCDIPFFGIQEEFNATLKGNLSFD 1039
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C;Species: Lytechinus variegatus (variegated urchin)
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T31437
R;Hertzler, P.L.; McClay, D.R.
submitted to the EMBL Data Library, May 1998
A;Description: Alpha SU2, a sea urchin integrin which binds laminin.
A;Reference number: 221035
                                                                                                                                                                                                                                          898 TE-----FQLELPVKYAVYMVVTS-----HGVSTKYLNFTASENTS---RVMQHQY
EHEMSQEGFSAAITSNGPLLSTVGSYDWAGGVFLYTSKEKSTFINMT-RVDSDMNDAYLG
                     YA--AAIILRNRVQSLVLGAPRYQHIGLVAMFR--QNTGMWESNANVKGTQIGAYFGASL
                                                                                             CSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPLPRGQRARWQCDAVLYGEQGQPWGRF
                                                                                                                                                                GAALIVLGDVNGDKLIDVAIGAPGEEDNRGAVYLFHGISGSGISPSHSQRIAGSKLSPRL
                                                                                                                                                                                                                                                                                                QYFGQSLSGGQDLTMDGLVDLTVGA--QGHVLLLRSQPVLRVKAIMEFNPREVARNVFBC
                                                                                                                                                                                                                                                                                                                                                                                                          483 HD------GQQPVNCLNVTTCFSFHGKHVPEEI---GLNYVLMADVAKKEKGQMPRVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                 F---NETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNFSL----VGTPLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           729 AFGNIRPVL----AEDAQRLFTALFPFEKNCGNDNICQDDLSITFSFM--SLD----CL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 778 VVGGPREFNVTVTVRNDGEDSYRIQVTFFPLDLSYRKVSTLQNQRSQRSWRLACESASS
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A;Title: Aberrant upregulation of a novel integrin alpha subunit gene at 3p21.3 in small A;Reference number: ISB409; MUD:94119603; PMID:8290272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PID:9533327
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A; Cross-references: NIPFOT: Q13797; GB:D25303; NID:g464180; PIDN:BAA04984.1; PID:g
A; Cross-references: UNIPFOT: Q13797; GB:D25303; NID:g464180; PIDN:BAA04984.1; PID:g
B; Palmer, E.L.; Ruegg, C.; Ferrando, R.; Pytela, R.; Sheppard, D.
J. Cell Biol. 123, 1289-1297, 1993
A; Title: Sequence and tissue distribution of the integrin alpha9 subunit, a novel paraference number: A49459; MUID:94064789; PMID:8245132
A; A; Crossion: A49459
A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1034 GNLSFDWYIKTSHNHLLIVSTAE-----ILFN------DSVFTLLPGQGAFVRSQTE 1079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------LPLIVGSSVGGLL 1103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C.Species: Homo sapiens (man)
C.Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
                                                                                                                                                754 NCGNDNICQDDLSIT--PSFM----SLDCLVVGGPREFNVTVTVRNDGEDSYRIQVTFFF
                                                                                                                                                                                                                          PLDLSYRKVSTLQNQRSQRSWRLACESASSTEVSGALKSTSCSINHPIFPENSEVTFNIT
                                   CFSYKGKEVPGYIVLFYNMSLDVNRKAESPPRFYFSSNGTSDVITGSIQVSSREANCRTH
                                                                                                 FDVDSKASLGNKLLLKANVTSEN--NMPRTNKTEFQLELPVKYAVYMVTSHGVSTKYLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                981 GIVRF---LSKTDKRLLYCIKADPHCLNFLCNFGKMESGKEASVHIQLEGRPS-ILEMDE
STRDRLREGQIQSVVTYDLALDSGR-----PHSRAVFNETKNSTRRQTQVLGLTQTCETL
                                                                          ----AFGNLRPVLAEDAQR-LFTALFPFEK
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10.7%; Score 630; DB 2; Length 1035;
Best Local Similarity 26.5%; Pred. No. 7.5e-35;
Matches 237; Conservative 160; Mismatches 332; Indels 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: integrin alpha-4 chain
C;Keywords: glycoprotein; metal binding; transmembrane protein
F;1-27/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                            GSNDENEPETCMVEKMNLTFHVINTGNSMAPNVSVEIMVPNSFS--
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                                                                          KLQLPNCIEDPVSPIVLRLNFSLVGTPLS-
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Residues: 30-1035 <PAL>;
Cross-references: GB:L24158
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1093 -LIVGSSVGGLLLLALITAALYKLGFFKR-----QYKDMMS--EGGPP 1132
                                                                                             Search completed: November Job time: 33.25 secs
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A;Status: preliminary; translated from GB/EWBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1041 <HER>
A;Residues: 1-1041 <HER>
A;Residues: 1-1041 of HER>
A;Experimental source: developmental stage embryo
C;Function:
A;Experimental source: davelopmental stage embryo
C;Function:
A;Description: binds laminin
C;Superfamily: integrin alpha-2b chain
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                                                                                                                                                                                                                                      QEGFSAAITSNGP--LLSTVGSYDWAGGVFLYTSKEKSTFINMTRVDS----DMNDAYLG 389
                                                                                                                                                                                                                                                             390 YAAAI--ILRNRVQSLVLGAPRYQHI-GLVAMFRQNTGMWESNANVKGTQIGAYFGASLC 446
                                                                                                                                                                                                                                                                                                                                                                                                      297 VVDI-NNDTYDDLLVGAPMYMDDGPAIQ------RWEAGAVYVYLQNPDVGPGA 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ::| : | | | : | : | : | CFTYTGNYLPDHIDISYTVTVDSGIIANRRAMFVDNDMSEIIKTRRLAVSTQFCDPLRAY 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LPNCIEDPVSPIVLRINFSLVGTPLSAFGN-----LRPVLAEDAQRLFTALFPFEK 753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         868 FDVDS-----KASLGNKLLLKANVTSENNMPRTNKTEFQLELPVKYAVYMVVTSHGVSTK 922
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                                                                                                                                                                                                       245;
                                                                                                                                                                 / Match 10.5%; Score 614.5; DB 2; Length 1041; Local Similarity 24.8%; Pred. No. 8.8e-34; Local Similarity 155; Mismatches 314; Indels 245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 893 YCASDSCVLINCTI-----DEINASKSKVVRILGRF---W-
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GenCore version 5.1.6
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OM protein - protein search, using sw model

November 9, 2004, 11:46:42; Search time 136.75 Seconds (without alignments) 4783.919 Million cell updates/sec Run on:

US-09-902-481B-6 5875 1 FNLDTENAMTFQENARGFGQ......FKRQYKDMMSEGGFPGAEPQ 1137 Title: Perfect score: Sequence:

1825181 segs, 575374646 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

UniProt\_02:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| -      | Description | P11215 homo sapien | mus m      | Q9ji30 rattus norv       | Q28984 sus scrofa | homo       | рошо       | mus m  | 83 m     | O9dxh4 mus musculu | 09qye7 rattus norv | P61625 bos taurus |            | pos    | 15 bo    | P24063 mus musculu |        | Q9r200 mus musculu |        |        |        | bos t  | O88340 rattus norv | Q60677 mus musculu | P38570 homo sapien | O88341 rattus norv | P56199 homo sapien | Q9ukx5 homo sapien | bos t      | Q62469 mus musculu | Q6p1c7 mus musculu | Aah65139 mus muscu |
|--------|-------------|--------------------|------------|--------------------------|-------------------|------------|------------|--------|----------|--------------------|--------------------|-------------------|------------|--------|----------|--------------------|--------|--------------------|--------|--------|--------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|------------|--------------------|--------------------|--------------------|
|        | ΠD          | ITAM HUMAN         | ITAM MOUSE | 0 <u>8</u> 11 <u>8</u> 0 | 028984            | ITAX HUMAN | ITAD HUMAN | Q6KAS4 | BAD21383 | ITAX MOUSE         | ITAD_RAT           | ITAL BOVIN        | ITAL HUMAN | QGTYBB | AAQ90015 | ITAL MOUSE         | Q9WTV4 | Q9R200             | Q98TF1 | Q98TF0 | Q96HB1 | QBHZV0 | 088340             | ITAE MOUSE         | ITAE HUMAN         | 088341             | ITA1 HUMAN         | ITAH HUMAN         | ITA2 BOVIN | ITA2 MOUSE         | Q6P1C7             | AAH65139           |
| :      | DB          | н                  | н          | 7                        | ~                 | Н          | П          | 7      | ~        | Н                  | н                  | н                 | 1          | 7      | 7        | Н                  | 7      | 2                  | ~      | ~      | 7      | 7      | 7                  | 7                  | H                  | C1                 | Н                  | Н                  | Н          | ٦                  | 7                  | 7                  |
|        | Length      | 1152               | 1153       | 1151                     | 920               | 1163       | 1162       | 1188   | 1188     | 1169               | 1161               | 1165              | 1170       | 1166   | 1166     | 1163               | 1161   | 1160               | 1196   | 1187   | 1086   | 927    | 1167               | 1167               | 1179               | 1167               | 2                  | 1189               | 1170       | 1178               | 1178               | 1178               |
|        | Match       | 9.66               | 76.2       | 74.7                     | 64.9              | 59.3       | 58.2       | 56.8   | 56.8     | 56.6               | 55.3               | 26.9              | 26.4       | 26.4   | 26.4     | 26.1               | 26.0   | 25.9               | 24.1   |        | 23.0   | ä      | 19.8               | ٠                  | 19.6               |                    |                    |                    | 18.5       |                    | 18.2               | 18.2               |
|        | score       | 5852.5             | 4476       | 4387                     | 3815.5            | 3483       | 3417       | 3335.5 | 3335.5   | 3326.5             | 3251.5             | 1578              | 1552.5     | 1552   | 1552     | 1533.5             | 1529.5 | 1519               | 1414   | 1363.5 | 1350.5 | 1270   | 1163.5             | 1157.5             | 1149               | 1119               | 10                 | 1093.5             | 1084       | 1072               | 1072               | 1072               |
| Result | . NO.       | Н                  | 7          | Э                        | 4                 | 5          | 9          | 7      | 80       | σ                  | 10                 |                   |            |        |          | 15                 |        | 17                 | 18     | 19     | 20     | 21     | 22                 | 23                 | 24                 | 25                 | 26                 | 27                 | 28         | 29                 | 30                 | 31                 |

| P17301 homo sapien<br>075578 homo sapien<br>P18614 rattus norv<br>P61622 mus musculu<br>07tqc3 mus musculu<br>042094 gallus gall<br>08bs01 mus sp. itg<br>08bwf4 felis silve<br>08bwf4 mus musculu<br>063001 rattus norv<br>069pg66 mus musculu | ממנים ווימים |
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| ITAZ HUMAN ITAG_HUMAN ITAI_RAT ITAI_RAT ITAH_MOUSE Q7TQG3 Q42094 Q8BS01 Q9WTP8 Q8TES5 Q8TES5 Q5PGG6 AAH57200  |              |
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## ALIGNMENTS

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J04145;
S52227;
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EMBL; S52154;
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granulocytes.
--- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins with I-domains do not undergo protease cleavage.
--- SIMILARITY: Belongs to the integrin alpha chain family.
--- SIMILARITY: Contains 7 FG-GAP repeats.
--- SIMILARITY: Contains 1 VWFA domain.
--- SIMILARITY: Contains 1 VWFA domain.
--- DATABASE: NAME=PROM; NOTE=CD guide CD11b entry;
--- WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cdllb.htm".
                                                                                                                                                                                                                            MEDLINE=87076671; PubMed=3539202; Pierce M.W., Remold-O'Donnell B., Todd R.F. III, Arnaout M.A.; Pierce M.W., Remold-O'Donnell B., Todd R.F. III, Arnaout M.A.; N.-terminal sequence of human leukocyte glycoprotein Mol: conservation across species and homology to platelet IIb/IIIa."; Biophys. Acta 874:368-371(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oxvig C., Springer T.A.,

"Experimental support for a beta-propeller domain in integrin alpha-
subunits and a calcium binding site on its lower surface.";

Proc. Natl. Acad. Sci. U.S.A. 95:4870-4875(1998).

-!- FUNCTION: Integrin alpha-M/beta-2 is implicated in various
adhesive interactions of monocytes, macrophages and granulocytes
as well as in mediating the uptake of complement-coated particles.

It is identical with CR-3, the receptor for the ic3b fragment of
the third complement component. It probably recognizes the R-G-D
peptide in C3b. Integrin alpha-M/beta-2 is also a receptor for
fibrinogen, factor X and ICAM1. It recognizes Pl and P2 peptides
of fibrinogen gamma chain.

-!- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-M
                                                                                                                                                                                                                                                                                                                                 Lee J.O., Rieu P., Arnaout M.A., Liddington R.; "Crystal structure of the A domain from the alpha subunit of integrin CR3 (CD11b/CD18)."; Cell 80:631-638(1995).
                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 148-334.
MEDLINE=5635671; Wubmed=8747460,
Lee J.O., Bankston L.A., Arnaout M.A., Liddington R.C.;
"Two conformations of the integrin A-domain (I-domain): a pathway for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98362595; PubMed=9687375;
Baldwin E.T., Sarver R.W., Bryant G.L., Tr., Curry K.A.,
Fairbanks M.B., Finzel B.C., Garlick R.L., Heinrikson R.L.,
Horton N.C., Kelley L.L., Middner A.M., Moon J.B., Mott J.E.,
Mutchler V.T., Tomich C.S., Watenpaugh K.D., Wiley V.H.;
"Cation binding to the integrin CD11b I domain and activation model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         associates with beta-2. SUBCELLULAR LOCATION. Type I membrane protein. TISSUE SPECIFICITION: Pre-Type I membrane protein monocytes and TISSUE SPECIFICITY: Pre-dominantly expressed in monocytes and
                                                  Shelley C.S., Arnaout M.A.;
"The promoter of the CD11b gene directs myeloid-specific and developmentally regulated expression.";
Proc. Natl. Acad. Sci. U.S.A. 88:10525-10529(1991).
                                                                                                                                               MEDLINE=92144986; PubMed=1346576;
Pahl H.L., Rosmarin A.G., Tenen D.G.;
"Characterization of the myeloid-specific CD11b promoter.";
Blood 79:865-870(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 148-337.
                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 148-331.
Proc. Natl. Acad. Sci. U.S.A. 86:257-261(1989).
                                                                                                                                                                                                                                                                                                                          MEDLINE=95171458; PubMed=7867070;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3D-STRUCTURE MODELING OF 17-616.
MEDLINE=98226734; PubMed=9560195;
                                        TEDLINE=92073318; PubMed=1683702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Structure 3:1333-1340(1995).
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                                                                                                                     SEQUENCE OF 1-9 FROM N.A.
                          SEQUENCE OF 1-9 FROM N.A
                                                                                                                                                                                                                 SEQUENCE OF 17-31.
                                                                                                                                     rissum=Blood;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00242; INTEGRIN_ALPHA; 1.
PROSITE; PS50234; VWFA; 1.
D-Structure; Calcium; Cell adhesion; Direct protein sequencing; Glycoprotein; Integrin; Magnesium; Receptor; Repeat; Signal; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GG; GO:0008305; C:integrin complex; TAS.
GG; GO:0007155; P:cell adhesion; TAS.
InterPro; IPR000413; Integrin_alpha.
InterPro; IPR0002035; WF A.
Pfam; PF01839; FG-GAP; 3.
Pfam; PF001839; FG-GAP; 3.
Pfam; PF00183; Integrin_alpha; 1.
PRINTS; PR01185; INTEGRINA.
PRINTS; PR01185; INTEGRINA.
SMART; SM00191; Int_alpha; 5.
SMART; SM00191; Int_alpha; 5.
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PDB; 1BHO; X-ray; 1/2=-.
PDB; 1BHO; X-ray; 1/2=-.
PDB; 1DDO; X-ray; 1/2=-.
PDB; 1IDO; X-ray; @=140-331.
PDB; 1UIM; X-ray; @=143-334.
PDB; 1MIM; X-ray; @=143-334.
PDB; 1MF7; X-ray; A=144-337.
PDB; 1NSZ; X-ray; A=140-335.
PDB; 1NAS; X-ray; A=140-335.
PDB; 1NAS; X-ray; A=140-335.
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AAA58410.1;
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AAA59903.1;
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| Db   976 RLNQTVIMDRPQVTFSENLSSTCHTKERLFSHSDFLAELRKAPVVNCSIAVCQRIQCDIP 1035   Oy   1021 FFGIQEENATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLPGQGAFVRSQTET 1080   | JUS<br>T  | OC EMERICALING FROMES:  ON MARMALIA: MATAZORS (MOUSE)  ON MARMALIA: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  ON NOBI TAXID=10090;  NO NO NOBI TAXID=10090;  NO NO NOBI TAXID=10090;  NO NO NOBI TAXID=10090;  NO NO NOBI TAXID=10 | RP SEQUENCE FROM N.A. (ISOFORM 2).  RP STRAIN=C57BL/6J; TISSUE=Spinal cord;  RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  RA Sazaki Y., Furuno W., Baito R., Suzuki H., Yamanaka I., Kiyosawa H.,  RA Saji K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Frazer K.S.,  RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Guschosy B.,  RA Gasterland S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D., | RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., RA Maglott D.R., Mattais L., Marchionni L., McKenzie L., Miki H., RA Magashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G., RA Petrovsky N., Pillai R., Pontius J.U., Oi D., Ramachandran S., RA avasi T., Reed J.C., Reed D.J., Reid J., Rang B.Z., Ringwald M., RA Sultana R., Takenhaw T., Taylor M.S., Teasdale R.D., Tomita M., RA Sultana R., Takenhaw T., Wahlestedt C., Wang Y., Watanabe Y., Wells C., RA Wilming L.G. Wynshaw Boris A., Yanagisawa M., Yang I., Yang L., RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K., RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato | RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Ra Hara A., Haahlzume W., Imochani K., Ishia Y., Itoh M., Kagawa I., RA Hara A., Haahlzume W., Imochani K., Shibata K., Shinagawa A., Sakali K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., RA Birney E., Hayashizaki Y.; RT Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; RL Nature 420:563-573(2002). RN SEQUENCE OF 11-45 FROM N.A. RC STRAIR=BALBA C.; IISSUB-Spleen; RN MEDLINE=BALBA C.; IISSUB-Spleen; RN MEDLINE=BALBA C.; IISDUB-Spleen; RA Sastre L., Roman J.M., Teplow D.B., Dreyer W.J., Gee C.E., Larson R.S., Roberts T.M., Springer T.A.; RT Partial genomic DNA clone for the alpha subunit of the mouse |
|---|---|--|---|---|---|
| FT SIGNAL 1 16  FT CHAIN 17 1152 Integrin alpha-M.  Query Match 99.6%; Score 5852.5; DB 1; Length 1152;  Best Local Similarity 99.6%; Pred. No. 0;  Matches 1132; Conservative 3; Mismatches 1; Indels 1; Gaps 1;  Qy   FNLDTENAMTPGENARGEGGSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSTGSCEPI 60 | Qy         61 RLQVPVEAVNMSLGLSLAAATTSPPQLLACGFTVHQTCSENTYVKGLCFLFGSNLRQOPQK 120           Db         77 RLQVPVEAVNMSLGLSLAATTSPPQLLACGFTVHQTCSENTYVKGLCFLFGSNLRQOPQK 136           Qy         121 FPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRWKEFVSTVMEQLKKSKTLFSLMQYSEEF 180           L37 FPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRWKEFVSTVMEQLKKSKTLFSLMQYSEEF 196           Qy         181 RIHFTFKEFQNNPNPRSLVKPITQLLGRTHTATGVRKVIRELINITNGARGNAFKILLVI 240           Qy         191 RIHFTFKEFQNNPNPRSLVKPITQLLGRTHTATGVRKVIRELINITNGARGNAFKILLVI 240           Db         197 PHPTFKFFQNNDNPDFGLYKPTTGLLGRTHTATGVRKVIRELINITNGARGNAFKILLVI 250 | 241 TDGEKFGDPLGYEDVIPEADREGVIRY/IGYGDAFRSEKSROELNTIASKPRDHVFGVN [  | 421<br>437<br>481<br>497<br>541<br>556  | QY         601 PULRVKAIMEENPREVARNVEECNDQVVKGKEAGEVRVCLHVQKSTRDRLAEGQIQSVVT 660           Db         616 PULRVXAIMEFNPREVARNVFECNDQVVKGREAGEVRVCLHVQKSTRDRLAEGQIQSVVT 675           QY         661 YDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNF 720           Db         676 YDLALDSGRPHSRAVENETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNF 735           CY         721 SLVQTPLSARGNERVLAEDRAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVG 795           Db         736 SLVGTPLSARGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVG 795   | QY         781 GPREFNUTVIVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEV         840           Db         796 GPREFNUTVIVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEV         855           QY         841 SGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRTNKTEF         900           Db         856 SGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRTNKTEF         915           QY         901 QLELPVKYAVYMVVTSHGVSTKYLNFTASENTSRVMQHQYQVSNLGQRSLPISLVFLVPV         960           Db         916 QLELPVKYAVYMVVTSHGVSTKYLNFTASENTSRVMQHQYQVSNLGQRSLPISLVFLVPV         975           QY         961 RLNQTVIWDRPQVFFSENLSSTCHTKERLPSHSRDYNVCSIAVCORIQCDIP         1020           QY         961 RLNQTVIWDRPQVFFSENLSSTCHTKERLPSHSBLRKAPVVNCSIAVCORIQCDIP         1020                 |

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Proc. Natl. Med. 65.4. U.S.A. 81:5644-5648 [1986].

Proc. Natl. Med. 65.4. U.S.A. 81:5644-5648 [1986].

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R GO; GO:0008305; C:integrin complex; IEA.

R GO; GO:0007160; P:cell-matrix adhesion; IEA.

R GO; GO:007229; P:integrin_mediated signaling pathway; IEA.

R InterPro; IPR00213; VWF.A.

R InterPro; IPR002035; VWF.A.

R Pfam; PF001839; FG-GAP; 2.

R Pfam; PF001839; FG-GAP; 2.

R Pfam; PF00327; VMF, 1.

R RINTS; PR01185; INTEGRINA.

R SMART; SM00191; Int alpha; 5.

R SMART; SM00191; Int alpha; 5.

R SMART; SM00192; VWFA; 1.

R PR0SITE; PS00242; INTEGRINA.

R PR0SITE; PS00242; INTEGRIN ALPHA; 1.

R PR0SITE; PS00242; INTEGRIN Transmembrane.

Cell adhesion; Integrin; Transmembrane.

SEQUENCE 1151 AA; 126943 WW; 8F785695D4074CA5 CRC64;
                                    IEA
                                                                                                                                                                                                                                                 Query Match 74.7%; Score 4387; DB 2; Best Local Similarity 73.1%; Pred. No. 1.9e-281; Matches 831; Conservative 146; Mismatches 158;
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                                                                        YDLALDSGRPHSRAVENETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNF
                                                                                                                                                                                                                                                                                                         GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR
                                                                                                                PRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLF
                                                                                                                                                                        HGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTVGAQGHVLLLRSQ
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Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1] —
SEQUENCE FROM N.A.
SETINALIAN D.M. Sr., Zerria K. Jr.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
-!- SIMILARITY: Belongs to the integrin alpha chain family.
EMBL; AF266593; AFR81280.1; -.
HSSP; P11215; 18HQ.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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VPVRLNQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQC 1017
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                     QVNNFEALKTIQNQLREKIFAIEGTQTGSSSSFEHEMSQEGFSAAITSNGPLLSTVGSYD
                                                                                                                                                      WAGGVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVA
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P20702; QSIVA6;
01-FEB-1991 (Rel. 17, Created)
01-CFEB-2004 (Rel. 44, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Integrin alpha-x precursor (Leukocyte adhesion glycoprotein p150,95
Integrin alpha chain) (Leukocyte adhesion receptor p150,95) (CD11C) (Leu M5)
Name=ITGAX; Synonyms=CD11C;
HGMC saplens (Human).
Bukaryota; Metacoa; Chodata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCEL_TAXID=9606;
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SEQUENCE FROM N.A.
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Lee J.-K., Schook L.B., Rutherford M.S.;
Lee J.-K., Schook L.B., Rutherford M.S.;
Lee J.-K., Schook L.B., Rutherford M.S.;
Lee J.-K., Schook L.B., Rutherford M.S.;
Lee J.-Subcattudar Location: The Emblank/DDBJ databases.
Lee J.-Subcattudar Location: The Emblank/DDBJ databases.
Lee Subcattudar Location: The Emblank/DDBJ databases.
Lee J.-K., Subcattudar Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Location: Lea Locati
                       SFNSKEIFNVTLQGNLLFDWYIETSHDHLLLVSTABILFNDSAFALLPGQETFVKAQTET
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     GPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEV
                                                                               SGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRTNKTEF
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Pred. No. 1e-243;
80; Mismatches 109; Indels
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
NCBI_TaxID=9823;
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Last annotation update)
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Cell adhesion, Integrin, Transmembrane.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins bowlan: The integrin I-domains do not undergo protease cleavage.

SIMILARITY: Belongs to the integrin alpha chain family.

SIMILARITY: Contains 7 FG-ABP repeats.

SIMILARITY: Contains NWFA domain.

DATABASE: NAME=PROW; NOTE=CD guide CD11c entry;

WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd11c.htm".
                      Corbi A.L., Miller L.J., O'Connor K., Larson R.S., Springer T.A., "CDM cloning and complete primary structure of the alpha subunit of a leukocyte adhesion glycoprotein, p150,95."; EMBO J. 6:4023-4028(1987).
                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=90153906; PubMed=2303426;
Corbi A.L., Garcia-Aguilar J., Springer T.A.;
"Genomic structure of an integrin alpha subunit, the leukocyte p150,95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: Integrin alpha-X/beta-2 is a receptor for fibrinogen. It recognizes the sequence G-P-R in fibrinogen. It mediates cell-cell interaction during inflammatory responses. It is especially important in monocyte adhesion and chemotaxis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 20-43.

MEDLINE=87167596; PubMed=3549901;
Miller L.J., Wiebe M., Springer T.A.;
"Purification and alpha subunit N-terminal sequences of human Mac-1 and pl50,95 leukocyte adhesion proteins.";
J. Immunol. 138:2381-2383(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             associates with beta-2.
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: Predominantly expressed in monocytes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                             rbi A.L., Garcia-Aguilar J., Springer T.A.;
Biol. Chem. 265:12750-12751(1990).
                                                                                                                                                                                                                                                                                                          molecule.";
J. Biol. Chem. 265:2782-2788(1990).
MEDLINE=88166645; PubMed=3327687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Blood
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or send an email to license@isb-sib.ch).

EMBL; M81695; AAA59180.1; -.

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Glycoprotein; Integrin; Magnesium; Polymorphism; Receptor; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Potential).
                                                                                                                                                                                                                                                                               3D-structure; Calcium; Cell adhesion; Direct protein sequencing;
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Extracellular (Potential).
Potential.
                                                                                                                                                                                                                                                                                                                                                       Cytoplasmic (Potential). FG-GAP 1. FG-GAP 2.
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T - S (in Ref. 4)

T - S (in Ref. 4)

T - S (in Ref. 4)

G - A (in Ref. 2)

E - K (in Ref. 2)

E - L (in Ref. 1)

I - V (in Ref. 1)
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GO; GO:0008305; C:integrin complex; TAS.
GO; GO:0004812; F:receptor activity; TAS.
GO; GO:0007155; P:cell adhesion; TAS.
GO; GO:0009887; P:crganogenesis; TAS.
InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; VWF.A.
Pfam; PP001839; FG-GAP; 3.
Pfam; PP00357; Integrin_alpha; 1.
Pfam; PP00925; VWA; 1.
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FG-GAP 4.
FG-GAP 5.
FG-GAP 6.
FG-GAP 7.
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PRINTS; PR00453; VWFADOMAIN.
SMART; SM00191; Int alpha; 5.
SMART; SM00327; VWA; 1.
PROSITE; PS00242; INTEGRIN_ALPHA; 1.
, M29465; -; NOT_ANNOTATED_CDS., M29487; AAA51620.1; ALT SEQ., M29482; AAA51620.1; JOINED., M29484; AAA51620.1; JOINED., M29484; AAA51620.1; JOINED., M29485; AAA51620.1; JOINED., M29486; AAA51620.1; JOINED.
 ANNOTATED CDS
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                                                                      EMBL, BC038237, AAH38237.1; -. PIR, A3584; RWHUIC. PDB; 1N3Y; X-ray; A=141-338. Genew; HGNC:6152; ITGAX.
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             PVLRVKAIMEFNPREVARNVFECNDQVVKGKEAGBVRVCLHVQKSTRDRLREGQIQSVVT
                                   PVLWVGVSMQFIPAEIPRSAFECREQVVSEQTLVQSNICLYIDKRSKNLLGSRDLQSSVT
                                                              YDLALDSGRPHSRAVFNETXNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNF
                                                                             SLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVG
                                                                                                                              TLVGKELLAFRNLREPLAADAQRYFTASLEFEKNCGADHICQDNLGISFSFPGLKSLLVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CD11d) (ADB2)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Integrin alpha-D precursor (Leukointegrin alpha)
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MEDLINE=20187620; PubMed=10722744;
Noti J.D., Johnson A.K., Dillon J.D.;
Gructural and functional characterization cane CD11d. Essential role of Spl and Sp3.";
J. Biol. Chem. 275:8959-8969(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1162 AA
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61.4%; Pred. No. 1.6e-221;
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                                                                                                                                                                                                                                                                                                                                       MEDLINE-99370002; PubMed=10438935;
MEDLINE-99370002; PubMed=10438935;
National Contern M., Crowe D.T., Hoekstra D., Vazeux R., Hoffman P.A.,
An der Vieren M., Crowe D.T., Hoekstra D., Vazeux R., Hoffman P.A.,
An der Vieren M., Crowe D.T., Hoekstra D., Vazeux R., Hoffman P.A.,
An drayson M.H., Bochner B.S., Gallatin W.M., Staunton D.E.;
The leukocyte integrin alpha D beta 2 binds VCAM-1: evidence for a
thinding interface between I domain and VCAM-1:,
J. Immunol. 163:1984-1990(1999)
C. I FUNCTION: Integrin alpha-D/beta-2 is a receptor for ICAM3 and
VCAM1. May play a role in the atherosolerotic process such as
clearing lipoproteins from plaques and in phagocytosis of blood-
borne pathogens, particulate matter, and senescent erythrocytes
clearing lipoproteins from plaques and in phagocytosis of blood-
borne pathogens, particulate matter, and senescent erythrocytes
clearing lipoproteins from plaques and a beta subunit. Alpha-D
associates with beta-2.
C. SUBURIT: Heterodimer of an alpha and a beta subunit. Alpha-D
associates with beta-2.
C. SUBCELLUIAR LOCATION: Type I membrane protein.
C. SUBCELLUIAR LOCATION: Type I membrane protein.
C. SUBCELLUIAR LOCATION: Type I membrane protein.
C. SUBCELLUIAR Location of palaques, and on splenic red pulp macrophages.
C. DOWAIN: The integrin I-domain (insert) is a VWFA domain. Integrins
C. SIMILARITY: Contains 7 FG-GAP repeats.
C. SIMILARITY: Contains 1 VWFA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                       MEDLINE=99059842; PubMed=9841932;
Grayson M.H., Van der Vieren M., Sterbinsky S.A., Michael Gallatin W.
Hoffman P.A., Stautton D.E., Bochner B.S.;
"alphadbeta2 integrin is expressed on human eosinophils and functions
                                                                                                                                                                                                                           an alternative ligand for vascular cell adhesion molecule 1 (VCAM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00242; INTEGRIN ALPHA; 1.
PROSITE; PS50234; VWFA; 1.
Calcium; Cell adhesion; Glycoprotein; Integrin; Magnesium; Receptor; Sfepeat; Signal; Transmembrane.
SIGNAL
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GO; GO:0008305; C:integrin complex; TAS.
GO; GO:001637; P:cell-cell adhesion; NAS.
GO; GO:0007160; P:cell-matrix adhesion; NAS.
GO; GO:000655; P:immune response; NAS.
InterPro; IPR000413; Integrin_alpha.
InterPro; IRR02035; WWF.A.
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EMBL, U40274; AAB60634.1; --
EMBL, U40275; AAB60635.1; --
EMBL, U40277; AAB60637.1; --
EMBL, U40277; AAB60637.1; --
EMBL, U40279; AAB60637.1; --
EMBL, U40279; AAB60638.1; --
EMBL, U40278; AAB60638.1; --
EMBL, P1278; AAB60638.1; --
EMBL, AF1078, AAB60638.1; --
EMBL, AF1078, AAB60638.1; --
EMBL, AF1078, AAB60638.1; --
EMBL, AF1078, AAB60638.1; --
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Pfam; PF00357; Integrin_alpha; 1.
                                                                                                                                                                                                                                                                                           J. Exp. Med. 188:2187-2191(1998)
[5]
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PRINTS; PR01185; IWPEGRINA.
PRINTS; PR00453; VWPADOMAIN.
SWART; SW00191; Int_alpha; 5.
SWART; SW00327; VWA; 1.
Gene 171:291-294 (1996)
   FARENT BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BETHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BERTHER BETHER BERTHER BERTHER BERTHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER BETHER
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78 PIHIRPEAVNMSLGLTLAASTNGSRLLACGPTLHRVCGENSYSKGSCLLLGSRW-EIIQT 136
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(Potential).
(Potential).
(Potential).
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                 Potential.
Cytoplasmic (Potential).
FG-GAP 1.
FG-GAP 2.
 Integrin alpha-D.
Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                    Match 58.2%; Score 3417; DB 1; Local Similarity 59.8%; Pred. No. 3.7e-217; es 675; Conservative 162; Mismatches 284;
                                                                                                                                            motif
                                                                                                                          Potential.
                                                                                                                                  Potential.
GFFKR moti
                                                                FG-GAP 3.
FG-GAP 4.
FG-GAP 5.
FG-GAP 6.
FG-GAP 7.
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7;

Gaps

19;

Length 1188; Indels

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458 QESRHWRPKSEVRGTQIGSYFGASLCSVDMDRDGGTDLVLIGVPHYYEHTRGGQVSVCPM
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                                                                                                                                                                                                                                                                                                                                                                                                                                               158 FPTAQQECPKQDQDIVFLIDGSGSISSTDFEKMLDFVKAVMSQLQRPSTRFSLMQFSDYF
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                                                                                                                                                                                            B8D93107BDBB4178
                                                                                                                                                                                                                          Query Match 56.8%; Score 3335.5; DB 2; Best Local Similarity 57.4%; Pred. No. 9.8e-212; Matches 654; Conservative 165; Mismatches 302;
                                                                                                                         PROSITE; PS00242; INTEGRIN_ALPHA; UNKNOWN_1.
PROSITE; PS50234; VWFA; 1.
Cell adhesion; Integrin; Transmembrane.
1 1 1 SEQÜENCE 1188 AA; 131248 MW; B8D93107BDB
          Pfam; PF01839; FG-GAP; 3.
Pfam; PF00357; Integrin_alpha; 1.
Pfam; PF00092; VWA; 1.
PRINTS; PR01185; INTEGRINA.
SMART; SM00191; Int_alpha; 5.
SMART; SM00327; VWA; 1.
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            PRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Res. 11:167-180(2004).
-!- SUBLELLULAR LOCATION: Type I membrane protein (By similarity).
-!- SIMILARRIY: Belongs to the integrin alpha chain family.
EMBL; AK131133; BAD21383.1; -.
GO; GO:0009897; C:external side of plasma membrane; IDA.
InterPro; IPR000413; Integrin alpha.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
MFLJ00114 protein (Fragment).
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                                                                                                                   QNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPL
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
05-JUL-2004 (Rel. 44, Last annotation update)
11tegrin alpha-X precursor (Leukocyte adhesion alpha chain) (Leukocyte adhesion receptor pls0,
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                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S., Okazaki N., Kitamura H., Nakagawa T., Nagase T., Ohara O., Koga H.; Saga Y., Kitamura H., Nakagawa T., Romose T., Ohara O., Koga H.; Prediction of the Coding Sequences of Mouse Homologues of FLJ Gene: The Complete Nucleotide Sequences of 110 Mouse FLJ-homologous cDNAs Identified by Screening of Terminal sequences of cDNA Clones RandomLy Identified D. Complete Name of Inbraries.";
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                                                               DVPVSINFWVPIELKGEAVW-TVMVSHPQNPLTQCYRNRLKPTQFDFLTHMQKSPVLDCS
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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Last annotation update)
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56.8%; Score 3335.5; DB 2;
Best Local Similarity 57.4%; Pred. No. 9.8e-212;
Matches 654; Conservative 165; Mismatches 302;
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BAD21383;
01-JUN-2004 (TrEMBLrel. 27,
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Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS, PRO1185; INTEGRINA.
PRINTS, PRO0453; VWFADOMAIN.
SWART; SM00191; Int_alpha; 5.
SWART; SM00327; VWA; 1.
PROSITE; PS00242; INTEGRIN_ALPHA; 1.
PROSITE; PS50234; VWFA; 1.
Calcium; Cell_adhesion; Glycoprotein; Magnesium; Receptor;
C., Rattis F.-M., Tseng S.-Y., Pardoll
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(Potential)
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MGD; MGI:96609; Itgax.
GO; GO:0009897; C:external side of plasma membrane; IDA.
InterPro; IPR00413; Integrin_alpha.
InterPro; IPR002035; WWF.A.
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Extracellular (Potential)
Potential.
Cytoplasmic (Potential).
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Pfam, PF00092; VWA; 1.
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                                                                                                                                                              FPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEF
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                                                                                        Gaps
                                                                                        19;
                                            Length 1169;
                                                                                        Indels
C616412033C219A6 CRC64;
                                         Score 3326.5; DB 1;
Pred. No. 3.8e-211;
                                                                                      Matches 652; Conservative 167; Mismatches 302;
                                            56.6%; Score 3326.5;
57.2%; Pred. No. 3.8e
129150 MW;
  1169 AA;
                                                                 Similarity
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                                              VCAMI. May play a role in the atherosclerotic process such as clearing lipoproteins from plaques and in phagosytosis of blood-borne pathogens, particulate matter, and senescent erythrocytes from the blood (By similarity).

SUBDINIT: Hererodimer of an alpha and a beta subunit. Alpha-D associates with beta-2 (By similarity).

SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins
                                                                                                                         1093 GOEAFLRACIKTVLEMYKVHNPVPLIVGSSVGGLLLLAIITAILYKAGFFKROYKEMLEE
                     IAVCQRIQCDIPFFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01839; FG-GAP; 3.
Pfam; PF00357; Integrin_alpha; 1.
Pfam; PF00357; Integrin_alpha; 1.
Pfam; PF000451; WA; 1.
PRINTS; PR01185; VWFADOMAIN.
SWART; SM00191; Int_alpha; 5.
SWART; SM00191; Int_alpha; 5.
PROSITE; PS00242; VWFA; 1.
PROSITE; PS50234; VWFA; 1.
Calcium; Cell adhesion; Glycoprotein; Magnesium; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Cloning of rat alpha D, a novel beta 2 integrin.";
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Integrin alpha-D/beta-2 is a receptor for ICAM3 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          with I-domains do not undergo protease cleavage.
SIMILARITY: Belongs to the integrin alpha chain family.
SIMILARITY: Contains 7 FG-GAP repeats.
SIMILARITY: Contains 1 WWFA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Sprague-Dawley;
O'Brien M.M., VanderVieren M., Kilgannon P.D., Dietsch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Integrin alpha-D.
Extracellular (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytoplasmic (Potential). FG-GAP 1.
                                                                                                                                                                                                                                                                                                        44, Last sequence update)
44, Last annotation update)
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InterPro; IPR000413; Integrin alpha.
InterPro; IPR002035; VWF.A.
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05-JUL-2004 (Rel. 44, Last seq
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                                                                                                                                                                                                                                                                                                                                                Integrin alpha-D precursor
                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -GVRGRWQCEATLHGEQGHPWGRFGVALTVLGDVNGDNLADVAIGAPGEEESRGAVYIFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 NLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSTGSCEPIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 IHFTFKEFONNPNPRSLVKPITQLLGRTHTATGVRKVIRELLNITNGARKNAFKILIVIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    200 THFTFTEFKNILDPQSLVDPIVQLQGLTYTATGIRTVMEELFHSKNGSRKSAKKILLVIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         362 VFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFRQ
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(Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                             (Potential)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                 FG-GAP 3.
FG-GAP 4.
FG-GAP 5.
FG-GAP 6.
                                                                                                                                                              Potential.
Potential.
GFFKR moti
                                                                                                                                         Potential
FG-GAP :
VWFA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QKFPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LQGHPGYQECIKGNVDLVFLFDGSMSLQQDEFEKIVDFMKDVMKKLSNSSYQFAAVQFST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     198 YFRTEFTELDYIRQKDPDALLAGVKHMRLLTNTFGAINYVAKEVFRPDLGARPDATKVLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 FNLDTENAMTFQENARG--FGQSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSTGSCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 PIRLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLRQQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EFRIHFTFKEFQNNPNPRSLVKPITQLLGRTHTATGVRKVIRELLNITNGARKNAFKILI
                                                                                                                                                          PROSITE; PS00242; INTEGRIN ALPHA; 1.
PROSITE; PS50234; VWFA; 1.
Calcium; Cell adhesion; Glycoprotein; Integrin; Magnesium; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Potential) (Potential) (Potential)
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                                                                                                                                                                                                                              Integrin alpha-L.
Extracellular (Potential)
                                                                                                                                                                                                                                                                     Cytoplasmic (Potential)
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(GlcNAc. . .)
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(GlcNAc. . .)
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                                                                                                                                                                                                                                                                                                                                                                                                                               GFFKR motif.

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Pred. No. 2.9e-95;
Contains 7 FG-GAP repeats.
Contains 1 VWFA domain.
                                                                                                                                                                                                                                                                                                                                                                             FG-GAP 7.
Potential.
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FG-GAP 2.
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                                                                                                                                                                                                                                                                                                              VWFA
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                                                                                                                                                                                                   Signal; Transmembrane
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                                                                                                                                               EMBL; AY267467; AAP94035.1;
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SIMILARITY:
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                                                                                                                                                                                                   854
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SUBGELLULA: Heterodimer of an alpha and a beta subunit. Alpha-L associates with beta-2 (By similarity).

SUBCELLULAR ICCATION: Type I membrane protein (By similarity).

DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins with I-domains do not undergo protease cleavage.

SIMILARITY: Belongs to the integrin alpha chain family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUL-2004 (Rel. 44, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
1ntegrin alpha-L precursor (Leukocyte adhesion glycoprotein LFA-1
alpha chain) (LFA-LA) (Leukocyte function associated molecule 1, alpha chain) (CD11a).
                                                                                                                                                                                      SPELTVIVIVWNEGEDSYGILVKFYYPAGLSYRRVIGTQ-QPHQYPLRLACEAEPAAQED
                                                                                                                                                                                                                                                --IRSSSCSINHPIFREGAKTTFMITFDVSYKAFLGDRLLLRAKASSENNKFDTNKTARQ
                                                                                                                                                                                                                                                                                                 LLKVELSIRFAPMEVAKAVYQCWERTPTVLEAGEATVCLTVHKGSPDLL--GNVQGSVRY
                                                                              LVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVGG
                                                                                                                                    PREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEVS
                                                                                                                                                                                                                            GALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRTNKTEFO
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                                                                                                                                                                                                                                                                                                                                    RLNQTVIWDRPQVTFSENLSS-TCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDI
            VLRVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRDRLREGO10SVVTY
                                                                DLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNFS
                                                                                                                                                                                                                                                                                                                                                                                           PFFGIQEEFNATLKGNLSFDWY1KTSHNHLLIVSTAEILFNDSVFTLLPGQGAFVRSQTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=ITGAL;
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
PubMed=14697514; DOI=10.1016/j.gene.2003.09.043;
Pett T., Zecchinon L., Baise E., Desmecht D.;
"The bovine (Bos taurus) CDIIa-encoding cDNA: molecular cloning, characterisation and comparison with the human and murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TKVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMM 1126
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Gene 325:97-101(
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                       310
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             546 GAVYIFNGQQG-GLSPRPSQRIEGTQMFSGIQWFGRSIHGVKDLGGDGLADVAVGAEGQV
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VITDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQ
                                              VNNFEALKTIONOLREKIFAIEGTOTGSSSSFEHEMSOEGFSAAITSNGPLLSTVGSYDW
                                                                                                                                       417 AMFRO--NTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGO
                                                                                                                                                                                    VSVCPL.PRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              939 QYQV----SNLGQRSLPISLVFLVPVRLNQTVI---WD---RPQVTFS-ENLSSTCHTKE
                                                                                          AGGVF-LYTSKEKSTFINMTRVDSDMNDAYLGYAAA-IILRNRVQSLVLGAPRYQHIGLV
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\_ITAL\_HUMAN STANDARD; PRT; 1170 AA.
P20701; 049746;
01-FEB-1991 (Rel. 17, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Integrin alpha-L precursor (Leukocyte adhesion glycoprotein LFA-1

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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J. Mol. Biol. 222:1-9(1999).
-!- FUNCTION: Integrin alpha-L/beta-2 is a receptor for ICAMI, ICAMZ,
-!- FUNCTION: Integrin alpha-L/beta-2 is a receptor for ICAMI, ICAMZ,
ICAM3 and ICAM4. It is involved in a variety of immune phenomena
including leukocyte-endothelial cell interaction, cytotoxic T-cell
mediated killing, and antibody dependent killing by granulocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             П
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-!- SIMILARITY: Belongs to the integrin alpha chain family.
-!- SIMILARITY: Contains 7 FG-GAP repeats.
-!- SIMILARITY: Contains 1 VWFA domain.
-!- DATABASE: NAME=PROW; NOTE=CD guide CD11a entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd11a.htm".
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM 1), AND PARTIAL SEQUENCE.
MEDLINE=89139587; PubMed=2537322;
Larson R.S., Corbi A.L., Berman L., Springer T.;
"Primary structure of the leukocyte function-associated molecule-1
"Primary structure of the leukocyte function-associated molecule-1
alpha subunit: an integrin with an embedded domain defining a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99425288; PubMed=10493852; Karlen J., Welzenbach K., Ramage P., Geyl D., Kriwacki R., Legge G., Cottens S., Weitz-Schmidt G., Hommel U.; Cottens S., Weitz-Schmidt G., Hommel W.; Structural basis for LFR-1 inhibition upon lovastatin binding to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 153-335, AND REVISION TO 214
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                                                                                                                 Euteleostomi;
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Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell Eichler E.E., Harris P.C., Venter J.C., Adams M.D.; Genome dublications and other features in 12 Mb of DNA s. Human chromose 16p and 16q.";
Genomics 60:295-108(1999).
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"Crystal structure of the I-domain from the CD11a/CD18
                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, E
Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               oŧ
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Note=No experimental confirmation available;
TISSUE SPECIFICITY: Leukocytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The role of the divalent cation in the structure "The role of the divalent cation in the structure
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SUBCELLULAR LOCATION: Type I membrane protein
ALTERNATIVE PRODUCTS:
Bvent-Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 153-334.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell Biol. 108:703-712(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 2)
                                   Name=ITGAL; Synonyms=CD11A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the CD11a/CD18 integrin.";
Structure 4:931-942(1996).
                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            integrin."
                                                                                                                                                                                   NCBI_TaxID=9606;
(CD11a).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  superfamily.
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PIRLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLR--- 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 LQGRPGFQECIKG----NVDLVFLFDGSMSLQPDEFQKILDFWKDVMKKLSNTSYQFAAV 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26 YNLDVRGARSFSPPRAGRHFGYRVLQV-GNGVIVGAPGE---GNSTGSLYQCQSGTGHCL 81
     Q -> QGVHGLVEMQISKQILCRPAGDAEHTVGAQEGELPC
PWGYSEAFRDNIRAGECR (in isoform 2).
FYIId=VSP 002738.
R -> W (in Ref. 1 and 2).
Y -> I (in Ref. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 295 HVFQVNNFEALKTIQNQLREKIFALEGTQTGSSSSFEHEMSQEGFSAAITSNGPLLSTVG
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                                                                                                                                                                                    Length 1166;
                                                                                                                                                                                                                                 Indels
                                                                                                                                         7B8D8AFBA896C9DF CRC64;
                                                                                                                                                                                    Query Match 26.4%; Score 1552; DB 2; Best Local Similarity 34.4%; Pred. No. 1.5e-93; Matches 407; Conservative 200; Mismatches 469;
PRINTS; PR00453; VWFADOMAIN.
SMART; SM00191; Int alpha; 5.
SMART; SM00327; VWA; 1.
PR05ITE; PS00242; INTEGRIN ALPHA; 1.
PR05ITE; PS50234; VWFR; 1.
Cell adhesion; Integrin; Transmembrane.
SEQUENCE 1166 AA; 128723 WW; 7B8D8A
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                                               GEEDNRGAVYLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTV
                                                                       GAQGHVLLLRSQPVLRVKAIMEFNPREVARNVFECNDQVV-KGKEAGEVRVCLHVQKSTR
                                                                                                                                                                                                                                                                                                                      EDPVSPIVLRINFSL---VGTPLS--AFGN-----LRPVLAEDAQRLFTALFPFEKNCGN
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                                                                                                                                                                                                                              DRIREGOIOSVVTYDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCI
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Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
-! SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
-! SIMILARATY: Belongs to the integrin alpha chain family.
EMBL; AX382558; AAQ90015.1; -.
Interpro; IPR000413; Integrin_alpha.
Interpro; IPR00139; FO-GAP; 1.
Pfam; PF01389; FO-GAP; 1.
Pfam; PF00357; Integrin_alpha; 1.
Pfam; PF00357; Integrin_alpha; 1.
Pfam; PF0189; VMA; 1.
Pfam; PF0189; VMA; I.
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Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Lymphocyte function-associated antigen 1 alpha subunit CDlla.
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1048 HLLIVSTAEILFNDSVFTLLPGQGAFVRSQTETKVEPFEVPNPLPLIVGSSVGGLLLLAL 1107
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01-MAR-1992 (Rel. 21, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Integrin alpha-L precursor (Leukocyte adhesion glycoprotein LFA-1
alpha chain) (LFA-1A) (Leukocyte function associated molecule 1, alpha chain) (CD11a).
                                                                                    : | | : : | | : : | | | : : | | HAPVGCEELPEEAVVHS-RALSCNVSSPIFGEDSMVDIQVMFNTLQKGSWGDFIELQANV
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     AMFRO--NTGMWESNANVKGTQIGAYFGASICSVDVDSNGSTDLVLIGAPHYYEQTRGGQ
                      VSVCPLPRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNR
                                                                                                                                    GAVYLFHGTSGSG1SPSHSQR1AGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTVGAQGHV
                                                                                                                                                                                                  LLLRSQPVLRVKAIMEFNPREVARNVFECNDQVVKGKEAG-EVRVCLHVQK--STRDRLR
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=91268976; PubMed=2051027;
Kaufmann Y., Tseng E., Springer T.A.;
"Cloning of the murine lymphocyte function-associated molecule-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1104 IFIALYKVGFFKRNLKEKMEANVDASSEIPGEDAGQPELEKE 1145
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SCNNEDSSLLEDNSATIS-----IPVMYPINVLTKDQENSTLYISFTPKSPRIHHVKH
                                                                        RLPSHSDFLAELRKAPVVNCSIAVCQRIQCDIPFFGIQEFNATLKGNLSFDWYIKTSHN
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                                                  SNLGQRSLPISLVFLVPVRLNQTVI---WD---RPQVTFS-ENLSSTCHTKE
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02-MAR-2004 (Triminante) 27, Last annotation update)
12-MAR-2004 (Triminante) 27, Last annotation update)
12-Maphocyte (unction-associated antigen 1 alpha subunit CD11a.
13-Mammalia; Butheriae).
13-Mammalia; Butheriae, Cetartiodactyla; Ruminantia; Pecora; Boviae; Boviae; Bos.
13-Mammalia; Bos.
13-MCBI_TaxID=9913;
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Dileepan T., Thumbikat P., Kannan M.S., Maheswaran S.K.;
Wholecular cloning and sequencing of bovine CD11a.";
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY382558; AAQ90015.1;
SEQUENCE 1166 AA; 128723 MW; 7B8DBAFBA896C9DF CRC64;
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                                                                                                                                      SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-Lassociates with beta-2.
SUBCELULAR LOCATION: Type I membrane protein.
SUBCELULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: Leukocytes.
DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins with I-domains do not undergo protease cleavage.
SIMILARITY: Belongs to the integrin alpha chain family.
SIMILARITY: Contains 7 FG-GAP repeats.
SIMILARITY: Contains 1 VWFA domain.
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Pfam; PF00357; Integrin_alpha; 1.
PROMS; VWA; 1.
PRONOS; VWA; 1.
PRINTS; PR0185; INTEGRINA.
PRINTS; PR0185; INTEGRINA.
PRINTS; PR00185; VWFADOMAIN.
SMART; SM00137; VWA; 1.
PROSITE; PS00242; INTEGRIN ALPHA; 1.
PROSITE; PS0234; VWFA; 1.
PROSITE; PS0234; VWFA; 1.
PROSITE; PS00387; VWFA; 1.
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Extracellular (Potential).
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oha-subunit and its expression in COS cells.";
Immunol. 147:369-374(1991).
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PIR, 156126, 156126.
HSSP, P20701, 1D60.
MGD, MGI:96606, Itgal.
InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; VWF_A.
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MEDLINE=85188276; PubMed=3887182;
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November 9, 2004, 11:45:42; Search time 103.25 Seconds (without alignments) 3950.365 Million cell updates/sec Run on:

US-09-902-481B-6 Title: Perfect score:

5875 1 FNLDTENAMTFQENARGFGG......FKRQYKDMMSEGGPPGAEPQ 1137 BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

2002273 seqs, 358729299 residues Searched:

2002273 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## CITAMARIC

| va        | Description           | Aaw65090 Human Bet | Aab07360 Human CD1 | Aau80252 Human int | Abg61469 Human Bet | 8        | Add25615 Binding d | Aar04136 Alpha sub | Adm99589 Human int | Adp12435 Protein e | Adp44061 Human CD1 | Adno2004 Human inf | Adq17510 Human sof |          | Aaw65091 Human Bet | Aab07361 Human CD1 | Abg61470 Human Bet | Abu07406 Protein d | Adg32005 Human hom |          | Aaw23049 Human bet | Aaw57491 Human bet | Aaw65089 Human Bet | Aaw72825 Human alp | Aaw73342 Human alp | Aab07359 Human alp |
|-----------|-----------------------|--------------------|--------------------|--------------------|--------------------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| SUMMAKIES | QI                    | AAW65090           | AAB07360           | AAU80252           | ABG61469           | AA014428 | ADD25615           | AAR04136           | ADM99589           | ADP12435           | ADP44061           | ADN02004           | ADQ17510           | AAR07120 | AAW65091           | AAB07361           | ABG61470           | ABU07406           | ADG32005           | AAR78166 | AAW23049           | AAW57491           | AAW65089           | AAW72825           | AAW73342           | AAB07359           |
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| æ         | Query<br>Match        | 99.9               | 6.66               | 6.66               | 99.9               | 6.66     | 99.9               | 99.7               | 9.66               | 99.5               | 59.4               | 59.1               | 59.1               | 59.0     | 58.7               | 58.7               | 58.7               | 58.7               | 58.7               | 58.2     | 58.2               | 58.2               | 58.2               | 58.2               | 58.2               | 58.2               |
|           | Score                 | 5868               | 98                 | 5868               | 5868               | 5868     | 98                 | S                  | LO                 | 5845.5             | 3487               | 3473               | 3473               | 3464     | 3450               | 3450               | 3450               | 3448               | 3448               | 3417     | 3417               | 3417               | 3417               | 3417               | 3417               | 3417               |
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| Abg61468 Human Bet<br>Aaw23064 Human bet<br>Aaw65106 Human Bet |                                  | Rat                              | Aaw60004 Rat alpha<br>Aaw72824 Rat alpha<br>Aab07374 Rat alpha | Abg61483 Rat Beta2<br>Aaw65104 Rat beta-<br>Aaw73345 Rat albha | Mo.                  | Aaw65103 Mouse bet<br>Aaw72836 Mouse alp<br>Aaw73347 Mouse alp |
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| ABG61468<br>AAW23064<br>AAW65106                               | AAW72837<br>AAW73343<br>AAB07376 | ABG61485<br>AAR78169<br>AAW23062 | AAW60004<br>AAW72824<br>AAB07374                               | ABG61483<br>AAW65104<br>AAW73345                               | AAW23061<br>AAW60003 | AAW65103<br>AAW72836<br>AAW73347                               |
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| 26<br>27<br>28   | 330<br>310<br>310                | 333                              | 35<br>37<br>37   | 3.9<br>8.0<br>9.0  | 422                  | 4 4 4<br>6 4 2   |

## ALIGNMENTS

Beta-integrin alpha-d subunit; human; modulator; treatment; psoriasis; type-I diabetes; atherosclerosis; multiple sclerosis; asthma; lung inflammation; acute respiratory distress syndrome; CD11b subunit; rheumatoid arthritis. Human Beta-integrin CD11b subunit protein. AAW65090 standard; protein; 1153 AA. (first entry) 28-SEP-1998 

sapiens. US5728533-A. Ношо

95US-00485618. 07-JUN-1995; 17-MAR-1998

93US-00173497. 94US-00286889. 94US-00362652. 23-DEC-1993; 05-AUG-1994; 21-DEC-1994;

(ICOS-) ICOS CORP.

Gallatin WM; WPI; 1998-206565/18. Van Der Vieren M,

Screening assay for modulators of integrin binding - using immobilised or labelled alpha-d polypeptide, useful for, e.g. treating type-I diabetes. Screening

Example 5; Fig 1A-D; 106pp; English.

This sequence represents a human beta-integrin CD11b subunit which is sued to describe a method for identifying compounds that modulate the interaction of the beta-integrin alpha-d subunit with a binding partner of alpha-d which involves contacting an alpha-d polypeptide with an alpha-d binding partner, one of which is immobilised and the other of which is labelled, in the presence of a test compound, and determining if the compound affects binding between the alpha-d polypeptide and alpha-d binding partner, where the alpha-d polypeptide is alpha-d or its fragment comprising the cytoplasmic, transmembrane or extracellular domain of alpha-d. Compounds that modulate alpha-d binding could be used to treat

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in cellular adhesion. Integrins are made up of an alpha subunit and a beta subunit. One class of human integrins are restricted to expression con which beta subunit. The leukcoyte structure blood cells and have a common beta2 subunit: the leukcoyte integrins, Leu-CAMs, leukcintegrins or beta2 integrins. Beta2 integrins can important role in immune and inflammatory responses. The present protein sequence is the human integrin alpha subunit CDILb. This sequence protein sequence is the human integrin alpha subunit CDILb. This sequence was used in an alignment to identify a novel beta2 integrin alpha cubunit; alpha d (AAA60014 and AAB07359). The present sequence has approximately $0% identity to the protein sequence of alpha_d. The capproximately $0% identity to the protein sequence of alpha_d. The approximately $0% identity to the protein sequence of alpha_d. The constant alpha d function e.g. Type I diabetes, atherosclerosis, multiple sclerosis, asthma, psoriasis, lung inflammation, acute respiratory (LAD). In addition, anti-alpha d monoclomal antibodies may be used in the inflation of macrophage inflateration at the site of a central nervous system injury. The monoclomal antibodies can also be used to detect and
                                                                                                                                                      1080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, macrophage infiltration inhibition, alpha d integrin, leukocyte integrin, Leu-CAM, leukointegrin, immune response, inflammation, leukocyte adhesion deficiency; LAD, Type I diabetes; atherosclerosis, multiple sclerosis, asthma; psoriasis, beta2 integrin, lung inflammation, acute respiratory distress syndrome; Crohn's disease; rheumatoid arthritis, central nervous system injury; CD11b.
                                                                                                                                                                                                                                                                                                                KVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMMSEGGPPGAEPQ 1137
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RINGTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDIP
                                                            RINOTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDIP
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This invention relates to a modified integrin-I or integrin I-like domain polypeptide comprising at least one disulfide bond so that the domain is stabilised in a desired conformation. The polypeptide of the invention may ave antiinflammatory or imunosuppressive activities. The invention of polypeptides of the invention have an open conformation and are useful as immunogens to produce antibodies that selectively bind to integrin I-domain, and for identifying a modulator of integrin activity, or of intearction of an integrin and a cognate ligand. The polypeptide of the invention, or antibodies (preferably anti-LFA-I antibody) is useful for invention, or autoimmune disorder in a subject and for inhibiting the binding of an integrin to a cognate ligand such as Crohn's disease, chiding of an integrin to a cognate ligand such as Crohn's disease, should not an integrin to a cognate ligand such as Crohn's disease, spinding of an integrin darthritis, dermatitis. A therapeutic composition comprising the peptide of the invention is useful for the integrin mediated disorder in a subject. The polypeptides
                                                 FFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTABILFNDSVFTLLPGQGAFVRSQTET 1096
                   FFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLPGQGAFVRSQTET 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and/or active or antigenic fragments are useful as reagents for diagnosis of integrin-mediated disorders. The present sequence represents the human integrin-1 alpha-M protein subunit used to generate the mutant polypeptides of the invention
                                                                                                                 KVEPFEVDNPLPLIVGSSVGGLLILALITAALYKLGFFKROYKDMMSEGGPPGAEPO 1153
                                                                                                                                                                                                                                                                                                                                                                               Integrin; antiinflammatory; imunosuppression; nephritis; dermatitis; inflammatory disease; autoimmune disorder; Crohn's disease; human immunodeficiency virus; HIV; myocardial infarction; Sjorgen's syndrome; rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified integrin-I or integrin I-like domain polypeptide useful as immunogen to produce antibodies specific to polypeptide, comprises disulfide bond such that polypeptide is stabilized in a desired
                                                                                             KVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMMSEGGPPGAEPQ
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                                                                                                                                                                                                                                                                                                                                             Human integrin 1 alpha-M subunit protein.
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                                                                                                                                                                                                                                                                                                  Beta2 integrin, alphaD subunit, CD11c subunit, CD11b subunit, LAD, leukocyte adhesion deficiency; inflammatory response; diabetes; multiple sclerosis, arthritis; graft atherosclerosis; neuroprotective; inflammatory bowel disease; Crohn's disease; ulcerative colitis; immune complex alveolitis; leukaemia; ICAM-R; vCAM-1; anti-inflammatory; intracellular cell adhesion molecule; vascular cell adhesion molecule; locomotor recovery; locomotor damage; locomotor impairment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Use of an anti-alpha-d monoclonal antibodies for promoting locomotor recovery, inhibiting locomotor damage, limiting locomotor impairment, or limiting autonomic and sensory dysfunction following spinal cord injury.
                                                                                     KVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMMSEGGPPGAEPQ 1137
                                                                                                       FFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTABILFNDSVFTLLPGQGAFVRSQTET
                                                       FFGIQEEFNATLKGNLSFDWY1KTSHNHLLIVSTAEILFNDSVFTLLPGQGAFVRSQTET
                                                                                                                                                                                                                                                                                                                                                                                                        autonomic dysfunction; sensory dysfunction; spinal cord injury.
                                                                                                                                                                                                                                                                          Human Beta2 integrin alphaCD11b subunit.
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The invention relates to promoting locomotor recovery, inhibiting autonomic and sensory definiting locomotor impairment, or limiting autonomic and sensory defunction following spinal cord injury by administering an anti-alpha d (Beta2 integrin alpha2 subunit) monoclonal antibody to a related form following spinal cord injury victim. The method also involves the use of a ligand spinal cord injury victim. The method also involves the use of a ligand selected from [CAM-N or VCAM-1 (intracellular cell adhesion molecule).

The method is useful for promoting commonic recovery, inhibiting locomotor damage, limiting locomotor inpairment, or limiting autonomic and sensory dysfunction following spinal cord injury. In particular, the spinal cord injury comprises compression of the spinal cord. The antibodies are also useful for reducing inflammation at the site of a central nervous system injury. The specification also details the identification of Beta2 integrins alphab cord inflammatory response, diabetes unalliple sclerosis, arthritis, graft atherosclerosis, inflammatory bowel disease, Crohn's disease, ulcerative collisis, immune complex alveolitis and leukaemia. The present sequence is a Beta2 integrin alpha protein sequence included for comparison with the Beta2 integrin alphab protein sequence

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1037 FFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLPGGGAFVRSQTET 1096
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Best Local Similarity 99.6%;
Matches 1133; Conservative
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                                                                                                                                                                                                                                                                           bioactive agent screening.
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                    Score 5868; DE
Pred. No. 0;
3; Mismatches
                    99.98;
                                      Matches 1133; Conservative
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Sequence 1153
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The invention comprises structurally biased variant integrin inserted (I) domain proteins, wherein the alterations to the protein occur in at least two noncontinuous regions. Specifically the the variant integrin I domain proteins are structurally biased to exist in the open conformation, thereby altering the binding ability of the protein. The invention also comprises nucleic acids encoding the variant integrin I domain proteins. The integrin I domain proteins and nucleic acids are useful for treating, preventing or suppressing integrin related inflammatory and immunological disorders (e.g. rheumatoid archritis). The variant integrin I domain proteins and nucleic acids con eused for treating: ischaemia/ reperfusion (e.g. hypovolemic shock); infarction; cerebral shock; viral infection; and cancer. The variant integrin I domain nucleic acids and infection; and cancer. The variant integrin I domain nucleic acids and
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                                                        1097 KVEPFEVPNPLPLIVGSSVGGLILLALITAALYKLGFFKRQYKDMMSEGGPPGAEPQ 1153
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KVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMMSEGGPPGAEPQ
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2002US-0385691P.
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                      FNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSTGSCEPI
                                             RLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLRQQPQK
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RESULT 7 AAR04136 g ठे g ò g ò 9  $\delta$ qq à pharmaceutical composition comprising the binding domain-immunoglobulin fusion protein or polynucleotide and a carrier, and treating a subject thaving or suspected of having a malignant condition or a B-cell disorder. The binding domain-immunoglobulin fusion protein is useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis, myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple solarosis or autoimmune disease. The present sequence is a binding domain -immunoglobulin fusion protein-associated protein sequence. Note: The sequence data for this patent formed part of the printed specification and is also available in electronic format directly from USPTO at sequence. The sequence in the printed specification by their SEQ ID number therefore none of the sequences can be explicitly identified. 360 RLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLRQQPQK 120 RLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLRQQPQK 136 240 300 316 436 480 376 GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR 420 496 540 556 919 949 720 SLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVG 796 92 FNLDTENAMTFGENARGFGGSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSTGSCEPI TDGEKFGDPLGYEDVI PEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVN NFEALKTIQNQLREKIFAIEGTQTGSSSSFEHEMSQEGFSAAITSNGPLLSTVGSYDWAG 377 GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR FNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSTGSCEPI PPBALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEF RIHFTFKEFQNNPNPRSLVKPITQLLGRTHTATGVRKVIRELLNITNGARKNAFKILIVI NFBALKTIQNQLREKIFAIEGTQTGSSSSFEHEMSQEGFSAAITSNGPLLSTVGSYDWAG QNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPL PRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLF PRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVA1GAPGEEDNRGAVYLF HGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTWDGLVDLTVGAQGHVLLLRSQ YDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNF SLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVG PVLRVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVT 0; Length 1153; 1; Indels 7; DB 3; Mismatches Score 5868; Pred. No. 0; 99.9%; Matches 1133; Conservative Local Similarity Sequence 1153 AA; 317 61 77 617 Query Match 17 121 137 181 197 241 257 301 421 437 481 497 541 557 601 661 721 361 QQ ò ద 원 g g g Ω ò à g à ò 8 qq ò Ωp  $\delta$ d ò Db  $\delta$ ò ò

RLNQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDIP 1020 RINGIVIMDRPQVIFSENLSSTCHTKERLPSHSDFLABLRKAPVVNCSIAVCQRIQCDIP 1036 FFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLPGQGAFVRSQTET 1080 900 960 KVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMMSEGGPPGAEPQ 1137 GPREFNVIVIVIVRNDGEDSYRIQVIFFFPLDLSYRKVSTLONORSQRSWRLACESASSTEV GPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEV SGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRTNKTEF SGALKSTSCSINHPIPPENSEVIFNITFDVDSKASLGNKLLLKANVTSENNMPRTNKTEF QLELPVKYAVYMVVTSHGVSTKYLNFTASENTSRVMQHQYQVSNLGQRSLPISLVFLVPV 391. 393
[1 abel = putative N-glycosylation site / 1abel = putative N-glycosylation site / 1abel = putative N-glycosylation site / 1abel = putative N-glycosylation site 697. 699
[1 abel = putative N-glycosylation site / 1abel = putative N-glycosylation site / 1abel = putative N-glycosylation site / 1abel = putative N-glycosylation site / 1abel = putative N-glycosylation site / 1abel = putative N-glycosylation site / 1abel = putative N-glycosylation site / 1abel = putative N-glycosylation site / 1abel = putative N-glycosylation site / 1abel = putative N-glycosylation site / 1abel = putative N-glycosylation site / 1abel = putative N-glycosylation site / 1abel = putative N-glycosylation site / 1abel = putative N-glycosylation site Mac-1 alpha subunit; Mac-1 alpha/beta heterodimer; non-specific defence system; integrin gene superfamily 86. .88 /label= putative N-glycosylation site Alpha subunit of Mac-1 leukocyte adhesion receptor /label= putative N-glycosylation 947. .949
[Jabel= putative N-glycosylation 979. .981
[Jabel= putative N-glycosylation 7] /label= putative N-glycosylation 901. .903 /label= putative N-glycosylation ...doel= putative N-glycosylation 941. .943
//label= putative N-glycosylation 240. .242 /label= putative N-glycosylation 1. .16 /label= signal\_peptide Ą. Location/Qualifiers AAR04136 standard; protein; 1153 (first entry) (revised) Modified-site Modified-site Modified-site Modified-site Modified-site Modified-site Modified-site 09-SEP-2004 Synthetic 797 841 857 917 977 1021 1037 1081 AAR04136; 781 901 961 Key Region 

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/label= putative N-glycosylation site 1022. .1024
/label= putative N-glycosylation site 1045. .1047
/label= putative N-glycosylation site 1051. .1053
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/label= putative N-glycosylation site 1076. .1078
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/label= putative_transmembrane_region
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Matches 1132; Conservative
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            GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR
                                    377 GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR
                                                                                          QNTGMMESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPL
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inflammatory bowel disease; multiple sclerosis; HIV; AIDS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel modified integrin protein having extracellular domains of integrin alpha and beta subunits or integrin alphaII and beta3 subunit, useful for treating integrin mediated disorders.
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Pred. No. 0;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 4; 232pp; English
                                             /note= "Encoded by CCC"
Location/Qualifiers
965
                                                                                                                                                                                                       17-JUL-2002; 2002US-0396783P.
17-JUL-2002; 2002US-0396790P.
11-SEP-2002; 2002US-0410135P.
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Best Local Similarity 99.6
Matches 1132; Conservative
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                                                                                                                                                                                                                                                                                             BLOOD RES
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N-PSDB; ADM99588.
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Misc-difference
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RINQTVIWDRPQVIPSENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDIP 1020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HIV entry inhibitor; cell surface protein inhibitor; HIV infection; anti-HIV; virucide; HIV uptake inhibitor; human; CD11C; integrin alpha X.
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HGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTWDGLVDLTVGAQGHVLLLRSQ
                            HGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTWDGLVDLTVGAQGHVLLLRSQ
                                                                                                             PVLRVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVT
                                                                                                                                                                  YDLALDSGRPHSRAVFNETKNSTRROTOVLGLTOTCETLKLOLPNCIEDPVSPIVLRLNF
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                                                                                 PVLRVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVT
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N-PSDB; ADP44060.
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                                                                                                                                                                                                                                                                                                                                                      The present invention relates to diagnosing or monitoring transplant rejection, e.g. cardiac or kidney transplant rejection, in an individual comprises detecting the expression level of one or more genes. The methods, system and kits are useful in diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, xenotransplant rejection or mechanical organ replacement rejection, in an individual. The method is also useful in assessing the immune status of an individual. The methods are also useful in diagnosing and monitoring an individual. The methods are also useful in diagnosing and monitoring lakeases that involve the immune system, e.g. rheumatoid arthritis, lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or viral, bacterial or fungal infection. The present sequence represents a protein that is encoded by the mRNA of the invention.
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Pred. No. 0;
3; Mismatches
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                                                                                                       Woodward R,
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                                                             (EXPR-) EXPRESSION DIAGNOSTICS
2002US-00131831.
2002US-00325899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 99.5%;
Matches 1131; Conservative
                                                                                                     Fry K,
                                                                                                                                                                    WPI; 2004-400724/37.
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                                                                                                       Wohlgemuth J,
  24-APR-2002;
20-DEC-2002;
                                                                                                                               Rosenberg S;
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The present invention describes a method (M1) for identifying an inhibitor of HIV entry into a human host cell. (M1) comprises identifying an inhibitor of HIV entry into a human host cell. (M1) comprises identifying an inhibitor of a cell surface polypeptide selected from CXCR-4 (352 amino acids, SEQ ID NO:10, ADP44061), CDA7 (353 amino acids, SEQ ID NO:10, ADP44061), CDA7 (353 amino acids, SEQ ID NO:10, ADP44061), CDA7 (353 amino acids, SEQ ID NO:16, ADP44063), CDB8 (354 amino acids, SEQ ID NO:18, ADP44065), CDB9 (199 amino acids, SEQ ID NO:20, ADP44065), CDB9 (199 amino acids, SEQ ID NO:20, ADP44067), CDA7 (565 amino acids, SEQ ID NO:20, ADP44071), RARA (462 amino acids, SEQ ID NO:20, ADP44071), PARA (462 amino acids, SEQ ID NO:20, ADP44071), PARA (462 amino acids, SEQ ID NO:30, ADP44071), CDA (462 amino acids, SEQ ID NO:30, ADP44071), PARA (462 amino acids, SEQ ID NO:30, ADP44071), PARA (462 amino acids, SEQ ID NO:30, ADP44071), PARA (462 amino acids, SEQ ID NO:30, ADP44081), Or PYEXB (1009 amino acids, SEQ ID NO:30, ADP44081), COR PYEXB (1009 amino acids, SEQ ID NO:30, ADP44081), COR PYEXB (1009 amino acids, SEQ ID NO:30, ADP44081), COR PYEXB (1009 amino acids, SEQ ID NO:30, ADP44081), COR PYEXB (1009 amino acids, SEQ ID NO:30, ADP44081), COR PYEXB (1009 amino acids, SEQ ID NO:30, ADP44081), COR PYEXB (1009 amino acids, SEQ ID NO:30, ADP44081), COR PYEXB (1009 amino acids, SEQ ID NO:30, ADP44081), COR PYEXB (1009 amino acids, SEQ ID NO:30, ADP44081), COR PYEXB (1009 amino acids, SEQ ID NO:30, ADP44081), COR PYEXB (1009 amino acids, SEQ ID NO:30, ADP44081), COR PYEXB (1009 amino acids, SEQ ID NO:30, ADP44081), COR PYEXB (1009 amino acids, SEQ ID NO:30, ADP44081), COR PYEXB (1009 amino acids, SEQ ID NO:30, ADP44081), COR PYEXB (1009 amino acids, SEQ ID NO:30, ADP44081), COR PYEXB (1009 amino acids, SEQ ID NO:30, ADP44081), COR PYEXB (1009 amino acids, SEQ ID NO:30, ADP44081), COR PYEXB (1009 amino acids, SEQ ID NO:30, ADP44081), COR PYEXB (1009 amino acids, SEQ ID NO:30, ADP44081), COR PYEXB (1009 amino acids a human host cell useful for preventing and/or treating HIV infection, identifying an inhibitor of a cell surface polypeptide such as CXCR-4. NO 14; 133pp; SEQ ID 

Sequence 1163 AA;

9 FNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSTGSCEPI Gaps ; 9 Length 1163; Query Match
Best Local Similarity 61.5%; Pred. No. 4.66-201,
Matches 694; Conservative 138; Mismatches 291; Indels

||||||| | FNLDTEELTAPRVDSAGFGDSVVQXANSWVVVGAPQKITAANQTGGLYQCGYSTGACEPI RLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLRQOPQK RIHFTFKEFQNNPNPRSLVKPITQLLGRTHTATGVRKVIRELLNITNGARKNAFKILIVI FPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEBF 198 20 61 121 ò 셤 g ð à d à g à

TDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVN 300 241

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301 NFEALKTIQNQLREKIFALEGTQTGSSSSFEHEMSQEGFSAALTSNGPLLSTVGSYDWAG DFDALKDIQNQLKEKIFAIEGTETTSSSSFELEMAQEGFSAVFTPDGFVLGAVGSFTWSG 318

1079 VRLNQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDI 1019 099 676 720 736 780 796 840 959 900 854 HGVLGPSISPSHSQRIAGSQLSSRLQYFGQALSGGQDLTQDGLVDLAVGARGQVLLLRTR ||||| || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || SLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVG GPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEV PVLRVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVT YDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNF 1020 PFFGIQEBFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLPGGGAFVRSQTE QLELPVKYAVYMVVTSHGVSTKYLNFTAS-ENTSRVMQHQYQVSNLGQRSLPISLVFLVP SGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRTNKTEF **QLELPVKYAVYTVVSSHEQFTKYLNFSESEEKESHVAMHRYQVNNLGQRDLPVSINFWVP** TKVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMMSE 661 855 915 096 601 617 677 721 737 781 797 841 901 975 1080  $\stackrel{>}{\sim}$ g ð qq ò qq à 8 ð 염 à qq à 셤 ð qq à g

ADN02004

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ADN02004 standard; protein; 1163

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ADN02004;

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197 240

(first entry) 17-JUN-2004 Human inflammatory bowel disease marker - CD11c protein.

Mip-1(beta); marker gene; inflammatory bowel disease; IBD; FcgammaR IIIa; FcgammaR IIIb; Mig; NRG-2; hexokinase; HM74; REG III; LPAP; MiL-selectin; EGELG; IDO; IL-8; CD11c; TLR2; ulcerative colitis; Crohn's disease. 

sapiens Ношо

360 317

377

JP2004065120-A.

04-MAR-2004

07-AUG-2002; 2002JP-00229705.

07-AUG-2002; 2002JP-00229705. (SUMU ) SUMITOMO SEIYAKU

Ä.

2004-209124/20.

N-PSDB; ADN01990

Novel marker gene of inflammatory bowel disease (IBD) comprising base sequence of e.g., Fc gamma R IIIa, Fc gamma R IIIb, Mig, NRG-2, hexokinase 3, HM74, CD11c, TLR2 gene, useful for screening therapeutic

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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN DESIGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-441208/41.
                                                                                                                                                                                                                                                                          tissue
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                                                                                                                                                                                                                                                                                                                                WO2004048938-A2.
                                                                                                                                                                                                                                                                                                               Homo sapiens
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                               The invention comprises marker genes for inflammatory bowel disease (IBI - FogammaR IIIa, FogammaR IIIb, Mig, NRG-2, hexokinase, HM74, REG III, LPAP, Mip-1 (beta), L-selectin, EGFL6, IDO, IL-8, CD11c, and THR2 genes. The DNA and protein sequences of the invention are useful in the detection and treatment of IBD (e.g. ulcerative colitis and Crohn's disease). The present amino acid sequence represents an IBD marker protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPREFNVTVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLONORSORSWRLACESASSTEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRGQRARWQCDAVI,YGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEBDNRGAVYLF
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                                                                                                                                                                                                              TDGEKFGDPLGYEDVI PEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVN
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                                                                                                                                                                                                                                                                                                                                                              GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR
                                                                                                                                                                                 FNLDTÉELTAFRVDSAGFGDSVVQYANSWVVVGAPQKITAANQTGGLYQCGYSTGACEPI
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                                                                                                                            Length 1163;
                                                                                                                                              Indels
                                                                                                                          59.1%; Score 3473; DB 8;
ilarity 61.3%; Pred. No. 6.9e-280;
Conservative 138; Mismatches 293;
                SEQ ID NO 27; 151pp; Japanese
                                                                                                                                      Similarity
                                                                                                           Sequence 1163 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
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                                              QLELPVKYAVYMVVTSHGVSTKYLNFTAS-ENTSRVMQHQYQVSNLGQRSLPISLVFLVP
                                                                                                                                                                                 960 VRLNQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDI
                                                                                                                                                                                                                                                                                                                PFFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLPGQGAFVRSQTE
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SGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRINKTEF
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Treatment of viral esp. rhino-viral infection - by admin. of alpha subunit of p150.95 cell surface adhesion receptor, opt. together with a beta chain of CD-18 family.
                                                                                                                                                                                                       p150,95 leucocyte adhesion receptor alpha-subunit; hairy cell leukaemia; rhinovirus.
                                      TKVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMMSF 1128
                                                               1143
                                                   p150.95 alpha subunit encoded by clone lambdax47.
                                                                                                                                                                                                                                                                                                                                        /label= glycosylation site 385. 387 / label= glycosylation site 392. 387. 1abel= glycosylation site 697. 699 / label= glycosylation site 735. 737 / label= glycosylation site 899. 901 / label= glycosylation site 904. 906 / label= glycosylation site 1050. 1052 / label= glycosylation site 1050. 1052 / label= glycosylation site 1050. 1052 / label= glycosylation site 1050. 1052 / label= glycosylation site 1068. 1133 / label= transmembrane
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                                                      RIHFTEKEFQNNPNPRSLVKPITQLLGRIHTATGVRKVIRELLNITNGARKNAFKILIVI
                                                                                                                                                                              NFEALKTIQNQLREKIFAIEGTQTGSSSSFEHEMSQEGFSAAITSNGPLLSTVGSYDWAG
                                         FNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSTGSCEPI
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     Length 1163;
                        Indels
59.1%; Score 3473; DB 8;
llarity 61.3%; Pred. No. 6.9e-280;
Conservative 138; Mismatches 293;
          Similarity
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Matches 692
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RNA extracted from phorbol myristate acetate stimulated HI-60 myelomonocytic cells. The library was screened with oligonuclectide probes based on tryptic peptide fragments of pi50.95. The sequence can be attached to appropriate control elements and expressed in prokaryotic and eukaryotic cells. The protein can be used to treat or prevent rhinoviral infection because it interacts with ICAM-1 and inhibits cell-virus attachment. It can also be used as an anti-inflammatory agent. See also AAQ06063-4, AAQ06068, AAR0711-8 and AAR07152-6. (Updated on 25-MAR-2003 to correct PR field.)
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lambda X47 was isolated from a cDNA library constructed from total
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Pred. No. 3.9e-279;
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61.1%;
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                                                                                                                                                                   Sequence 1163 AA;
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GPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEV 840 

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This sequence represents a human beta-integrin CDIIc subunit which is used to describe a method for identifying compounds that modulate the interaction of the beta-integrin alpha-d subunit with a binding partner of alpha-d which involves contacting an alpha-d polypeptide with an alpha-d binding partner, one of which is immobilised and the other of which is labelled, in the presence of a test compound, and determining if the compound affects binding between the alpha-d polypeptide and alpha-d binding partner, where the alpha-d polypeptide is alpha-d or its fragment comprising the cytoplasmic, transmembrane or extracellular domain of alpha-d alseases such as type-I diabetes, atherosclerosis, multiple sclerosis, asthma, psoriasis, lung inflammation, acute respiratory distress syndrome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Beta-integrin alpha-d subunit; human; modulator; treatment; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              type-I diabetes; atherosclerosis; multiple sclerosis; asthma; lung inflammation; acute respiratory distress syndrome; CD11c subunit;
                                                                                 1020 PPFGIQEBFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLPGQGAFVRSQTE
                                                                                                                                                                                                          SQGTWSTSCRINHLIFRGGAQITFLATFDVSPKAVLGDRLLLTANVSSENNTPRTSKTTF
                                                                                                                         960 VRLNOTVIWDRPOVIFSENLSSTCHIKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDI
                                                                                                                                           SGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRTNKTEF
                                                            OLELPVKYAVYMVVTSHGVSTKYLNFTAS-ENTSRVMOHOYQVSNLGQRSLPISLVFLVP
                                                                                                                                                                                                                                                1080 TKVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMMSE 1128
                                                                                                                                                                                                                                                                  Human Beta-integrin CD11c subunit protein.
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and rheumatoid arthritis
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                        Length 1163;
                                         Indels
              Query Match
Best Local Similarity 61.0%; Fred. No. 5.7e-278;
Matches 689; Conservative 144; Mismatches 290;
Sequence 1163 AA;
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PFFGIQEEFNATLKGNLSFDMYIKTSHNHLLIVSTAEILFNDSVFTLLPQQGAFVRSQTE 1079
                                                                                                                                        Human; macrophage infiltration inhibition; alpha_d integrin; leukocyte integrin; Leu-CAM; leukointegrin; immune response; inflammation; leukocyte adhesion deficiency; LAD; Type I diabetes; atherosclerosis; multiple sclerosis; asthma; psoriasis; beta2 integrin; lung inflammation; acute respiratory distress syndrome; Crohn's disease; rheumatoid arthritis; central nervous system injury; CDILC.
         TKVEPFEVPNPLPLIVGSSVGGLLLLLALITAALYKLGFFKRQYKDMMSE
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                                                                                  protein; 1163
                                                                                                                          Human CD11c protein sequence.
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Vieren M; 98US-00193043 99US-00350259 Van Der CORP Gallatin MW, (ICOS-) ICOS 16-NOV-1998; 08-JUL-1999;

99WO-US027139

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25-MAY-2000

WO200029446-A1.

WPI; 2000-387751/33.

use of novel anti-alpha integrin d monoclonal antibodies to inhibit macrophage infiltration and reduce inflammation at central nervous system injury sites.

Example 5; Fig 1; 270pp; English.

Integrins are a class of membrane-associated molecules that participate in cellular adhesion. Integrins are made up of an alpha subunit and a beta subunit. One class of human integrins are restricted to expression in white blood cells and have a common beta2 subunit: the leukcyte can in white blood cells and have a common beta2 subunit: the leukcyte beta2 integrins. Leu-CAMS, leukcintegrins or beta2 integrins. Beta2 integrins conversed in an important role in immune and inflammatory responses. The present conversed in an alignment to identify a novel beta2 integrin alpha conversed in an alignment to identify a novel beta2 integrin alpha approximately 66\* identity to the protein sequence has approximately 66\* identity to the protein sequence of alpha d. The Alpha d gene and protein may be useful in therapy for diseases linked to aberrant alpha d function e.g. Type I diabetes, atherosclerosis, multiple constress syndrome, rheumatoid arthritis and leukcoyre adhesion deficiency confinibition of macrophage infiltration at the site of a central nervous confinibition of macrophage infiltration at the site of a central nervous and an antipa of the confining the confining of the confining and leukcoyre adhesion and the site of a central nervous confining or the confining and leukcoyre adhesion and confining and confining and protein and conclours and the site of a central nervous confining the confining and protein and the site of a central nervous confining and protein and confining

Sequence 1163 AA;

Score 3450; DB 3; Length 1163; Pred. No. 5.7e-278; 58.7%; Query Match Best Local Similarity

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9, 2004, 12:08:29 Search completed: November Job time : 108.25 secs

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Sequence 1, Appli
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Sequence 30, Appl
Sequence 176, Appl
Sequence 5, Appli
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Sequence 204, Appl
Sequence 4, Appli
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4119.157 Million cell updates/sec
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US-09-350-259-3
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4 US-10-207-655-176
0 US-09-902-401A-5
US-09-902-401A-5
0 US-09-902-401A-3
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0 US-09-902-401A-3
0 US-09-350-259-4
0 US-09-902-401A-3
0 US-09-350-259-4
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GenCore version
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                                                      OM protein - protein search, using sw model
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Listing first 45 summaries
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| Sequence 6, Application US/09902481A
| Publication No. US20030054440A1
| GENERAL INFORMATION
| APPLICANT: Springer, Timothy
| APPLICANT: Shimaoka, Motomu
| APPLICANT: Shimaoka, Motomu
| APPLICANT: Shimaoka, Motomu
| APPLICANT: Shimaoka, Motomu
| APPLICANT: Shimaoka, Motomu
| APPLICANT: Shimaoka, Motomu
| TITLE OF INVENTION: NOVEL PROTEINS WITH INTECRIN-LIKE ACTIVITY
| CURRENT APPLICATION NUMBER: US/09/902,481A
| CURRENT FILING DATE: 2001-07-09
| PRIOR PILING DATE: 2000-07-07
| NUMBER OF SEQ ID NOS: 7
| SOFTWARE: Patentin version 3.1
| IENGTH: 1137
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9 US-09-350-259-53
10 US-09-360-259-53
110 US-09-360-259-53
110 US-09-360-259-37
110 US-09-360-259-37
110 US-09-360-259-46
120 US-09-891-943-46
130 US-09-891-943-46
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130 US-09-891-943-101
130 US-09-350-259-103
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100.0%; Pred. No. 0;
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ORGANISM: Artificial sequence
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APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TILE OF INVENTION: NO. US2002062008Alel Hum
FILE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/350,259
CURRENT FILING DATE: 1999-07-08
EARLIER FILING DATE: 1993-12-23
EARLIER FILING DATE: 1993-12-3
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-08-05
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EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-10-03
NUMBER OF SEQ ID NOS: 114
                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1133; Conservative 3; Mismatches
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ORGANISM: Homo sapiens
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                                                                                                                                                                      GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR
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                                              TDGBKFGDPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVN
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RESULT 2 US-09-350-259-3 ; Sequence 3, Application US/09350259

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                                                       GPREFNYTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEV
677 YDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNF
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APPLICANT: Li, Rui
APPLICANT: Xiong, Jian-Ping
APPLICANT: Xiong, Jian-Ping
APPLICANT: Xiong, Jian-Ping
APPLICANT: Xiong, Jian-Ping
TITLE OF INVENTION: VARIANT INTEGRIN POLYPEPTIDES AND USES THEREOF
FILER REFERENCE: 00768-54801
CURRENT APPLICATION NUMBER: US/10/144,259
CURRENT FILING DATE: 2002-09-04
PRIOR FILING DATE: 2001-01-11
PRIOR FILING DATE: 2001-01-11
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FASLSEQ for Windows Version 4.0
SEQ ID NO 30
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99.6%; Pred. No. 0;
tive 3; Mismatches
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Publication No. US20030109691A1
GENERAL INFORMATION:
APPLICANT: Arnaout, M. Amin
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Best Local Similarity 99.6
Matches 1133; Conservative
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ORGANISM: Homo sapiens
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US-10-144-259-30
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                                  GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: NO. US20030077278Alel Hum
TITLE OF INVENTION: NO. US20030077278Alel Hum
FILE REFERENCE: 27866/35004
CURRENT FILING DATE: 2001-06-26
CURRENT FILING DATE: 1998-11-16
PRIOR FILING DATE: 1994-08-05
PRIOR FILING DATE: 1994-08-05
PRIOR FILING DATE: 1994-12-21
PRIOR FILING DATE: 1994-12-21
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PRIOR FILING DATE: 1994-12-21
PRIOR FILING DATE: 1994-12-3
PRIOR FILING DATE: 1994-12-3
SPRIOR FILING DATE: 1994-12-3
SPRIOR FILING DATE: 1994-12-3
SPRIOR FILING DATE: 1997-10-03
SPRIOR FILING DATE: 1997-10-03
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Best Local Similarity 99.6
Matches 1133; Conservative
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CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
SOFTWARE: Patentin version 3.0
SEQ ID NO 176
LENGTH: 1153
                                                                                       Best Local Similarity 99.6
Matches 1133; Conservative
                                                           sapiens
                                                  TYPE: PRT
ORGANISM: Homo
                                                               US-10-207-655-176
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               TOGEKFGDPLGYEDVI PEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVN
                         NFEALKTIQNQLREKIFAIEGTQTGSSSSFEHEMSQEGFSAAITSNOPLLSTYGSYDWAG
                                                        GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR
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                                                                                          QUIGNWESNANVKGTQIGAXFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPL
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APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION |
FILE REFERENCE: 390069.401C1
CURRENT APPLICATION NUMBER: US/10/207,655
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Publication No. US20030118592A1
GENERAL INFORMATION:
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US-10-207-655-176
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                                        FNLDTENAMTFOENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSTGSCEPI
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Pred. No. 0;
3; Mismatches
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AND METHODS FOR PRODUCING SAME
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                                                        PRGORARWOCDAVLYGEOGOPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLF
                  ONTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCFL
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APPLICANT: Springer, Timothy A. APPLICANT: Shimacka, Motomu APPLICANT: Lu, Chafen; TITLE OF INVENTION: MODIFIED POLYEPTIDES STATITIC OF INVENTION: DESTRED CONFORMATION NUMBER: US/09/945,265; CURRENT APPLICATION NUMBER: US 60/229,700; PRIOR APPLICATION NUMBER: US 60/229,700; PRIOR APPLICATION NUMBER: US 60/229,700; PRIOR APPLICATION NUMBER: US 60/229,700; NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 4;
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        QLELPVKYAVYMVVTSHGVSTKKINFTASENTSRVMQHQYQVSNLGQRSLPISLVFLVPV
                                                            RLNOTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDIP
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                     APPLICANT: Springer, Timothy
APPLICANT: Springer, Motomu
APPLICANT: Shifman, Julia
APPLICANT: Shifman, Julia
APPLICANT: Shifman, Julia
APPLICANT: Shifman, Julia
APPLICANT: Shifman, Julia
APPLICANT: Shifman, Julia
APPLICANT: Shifman, Julia
APPLICANT: MAYO, Stephen
TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
FILE REFERENCE: A-70586-1/RFT/RMS/RMK
FILE REFERENCE: A-70586-1/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US 60/216,600
PRIOR APPLICATION NUMBER: US 60/216,600
PRIOR FILING DATE: 2001-07-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO 5.
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Pred. No. 0;
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ORGANISM: Artificial sequence
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Best Local Similarity 99.1%;
Matches 1127; Conservative
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Sequence 4, Application US/09902481A

Publication No. US2030054440A1

APPLICANT: Springer, Timothy
APPLICANT: Shimacka, Motomu
APPLICANT: Shiman, Julia
APPLICANT: Mayo, Stephen
ITITE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
CURRENT FILLS PATOS86-1/RFT/RMS/RMK
CURRENT FILLS DATE: 2001-07-09

PRIOR FILLING DATE: 2001-07-09

PRIOR FILLING DATE: 2000-07-07

NUMBER OF SEQ ID NOS: 7

SOFTWARE: Patentin version 3.1

SEQ ID NO 4

LUMBER OF SEQ ID NOS: 7

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99.0%; Pred. No. 0;
tive 8; Mismatches
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ORGANISM: Artificial
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Best Local Similarity
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                                                             FNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLXQCDYSTGSCEPI
                                                                                 RLQVPVEAVNMSIGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLRQQPQK
                                                                                            PPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEF
                                        FNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDXSTGSCEPI
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                                                                                                                           GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR
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                                     FPEALRGCPQEDSDIAFLIDGSGS11PHDFRRMKEFVSTVMBQLKKSKTLFSLMQYSEEF
                                                                           RIHFTEKEFONNPNPRSLVKPITQLLGRIHTATGVRKVIRELLNITNGARKNAFKILIVI
           RLOVPVBAVNMSLGLSLAATTSPPQLLACGPTVHQTCSBNTYVKGLCFLFGSNLRQQPQK
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  PVLRVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVT
                                                    APPLICANT: Sprinacka, Motomu APPLICANT: Sprinacka, Motomu APPLICANT: Shifman, Julia APPLICANT: Shifman, Julia APPLICANT: Shifman, Julia APPLICANT: Shifman, Julia APPLICANT: Mayo, Stephen APPLICANT: Mayo, Stephen TILE REPERENCE: A-70586-1/RFT/RMS/RMK FILE REPERENCE: A-70586-1/RFT/RMS/RMK CURRENT APPLICANTION NUMBER: US/09/902,481A CURRENT FILING DATE: 2001-07-09 PRIOR FILING DATE: 2001-07-07 PRIOR FILING DATE: 2000-07-07 SOFTWARE: Patentin version 3.1 SEQ ID NO 3 SEQ ID NO 3 LENGTH: 1137
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Pred. No. 0;
9; Mismatches 6;
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Best Local Similarity 98.7%;
Matches 1122; Conservative
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61.0%; Pred. No. 5.3e-282;
Live 144; Mismatches 290;
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APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Michael W.
APPLICANT: Wan der Vieren, Monica
FILE REFERENCE: 27866/3504
CURRENT APPLICATION WUMBER: US/09/350, 259
CURRENT FILING DATE: 1999-07-08
EARLIER PILING DATE: 1999-11-16
EARLIER FILING DATE: 1993-12-23
EARLIER FILING DATE: 1993-12-23
EARLIER FILING DATE: 1994-12-23
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1994-10-03
NUMBER OF SEQ ID NOS: 114
SOFFWARE: PALENTING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
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ORGANISM: Homo sapiens
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                                                                     APPLICANT: Blan Pharmaceutical Technology
APPLICANT: Brayden, David
APPLICANT: Brayden, David
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APPLICANT: Brayden, David
APPLICANT: Brayden, David
APPLICANT: Heabkin, Imelda
APPLICANT: Lambkin, Inselda
APPLICANT: Lambkin, Lisa
TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and Methods and
TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cells and Methods and
TITLE OF INVENTION: MUMBER: US/10/116,275
UURRENT APPLICATION NUMBER: US/10/116,275
NUMBER OF SEQ ID NOS: 349
SOFTWARE: Patentin version 3.1
SEQ ID NO 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 RLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLRQQPQK 120
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                                                                                                                                                                                                                                                                                                                                                                         Query Match

S9.1%; Score 3473; DB 14; Length
Best Local Similarity 61.3%; Pred. No. 6e-284;
Matches 692; Conservative 138; Mismatches 293; Indels
                           Sequence 204, Application US/10116275
Publication No. US20030211476A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
RESULT 11
US-10-116-275-204
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RESULT 13 US-09-891-943-4 ; Sequence 4, Application US/09891943

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APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. US20030077278Alel Hum
FILE REFERENCE: 27866/35004
CURRENT APPLICATION UNDHER: US/09/891,943
CURRENT APPLICATION NUMBER: 09/193,043
PRIOR FILING DATE: 1998-11-16
PRIOR FILING DATE: 1998-11-16
PRIOR FILING DATE: 1998-10-26
PRIOR FILING DATE: 1994-08-05
PRIOR FILING DATE: 1994-08-05
PRIOR FILING DATE: 1994-08-05
PRIOR FILING DATE: 1994-08-05
PRIOR FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PARENTIN VET: 2.0
SEQ ID NO 4
SEQ ID NO 4: 16-22 ORGANISM: Homo sapiens LENGTH: 1163 US-09-891-943-4 481 498 601 199 541 61 138 198 241 258 361 421 438 181 301 20 121 TYPE: PRT d ö ₽

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US-09-891-943-2
; Sequence 2, Application US/09891943
; Publication No. US20030077278A1
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SNLELNAEVWVWNDGEDSYGTTITFSHPAGLSYRYVAEGQXQGLRSLHLTC--CSAPVG
                                SLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVG
                                                GPREFNVIVIVRNDGEDSYRTQVTFFFPLDLSYRKVSTLONQRSQRSWRLACESASSTEV
                                                                                                                        SGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRINKTEF
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                                                                                                                                                                                                                                                                                                     TKVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKROYKDMMSF 1128
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SQ1930-239-2
SQ1930-239-2
Fatent No. US20020062008A1
GENERAL INFORMATION:
FAPELICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. US20020062008A1el Hum
FITLE REFERENCE: 27866/3504
CURRENT APPLICATION NUMBER: US/09/350,259
CURRENT FILING DATE: 1999-07-08
EARLIER APPLICATION NUMBER: 09/13,497
EARLIER PILING DATE: 1999-11-16
EARLIER PILING DATE: 1994-12-23
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1994-10-03
SQ1D NOS: 114
SSCID NOS: 114
SSCID NOS: 114
SSCID NOS: 114
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US-09-350-259-2
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                                                                                                                                                                                                                                                                    Length 1161;
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58.2%; Score 3417; DB 10;
Best Local Similarity 59.8%; Pred. No. 3.3e-279;
Matches 675; Conservative 162; Mismatches 284;
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                           Human
GENERAL INFOGRATION:
GENERAL INFOGRATION:
APPLICANT: GAILatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITIER OF INVENTION: NO. US20030077278A1el Hunr
TITIER PREPERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/891,943
CURRENT APPLICATION NUMBER: 09/193,043
PRIOR PRILING DATE: 1998-11-16
PRIOR FILING DATE: 1998-11-2
PRIOR PILING DATE: 1994-12-21
PRIOR FILING DATE: 1994-12-21
PRIOR FILING DATE: 1994-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PATENTIN UNBER: 08/343,363
PRIOR FILING DATE: 1997-10-03
SOFTWARE: PATENTIN UNBER: 1997-11-10-03
SOFTWARE: PATENTIN UNBER: 1897-11-10-03
SOFTWARE: PATENTIN UNBER: 1897-11-10-03
SOFTWARE: PATENTIN UNBER: 1897-11-10-03
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US-09-891-943-2
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1020 PFFGIQEBFNATLKGNLSFDWYIKTSHNHLLIVSTABILFNDSVFTLLPGGGAFVRSQTB 1079
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                                                                                                                     GPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEV
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674 FDLALDPGRLTSRAIFNETKNPTLTRRKTLGLGIHCETLKLLLPDCVEDVVSPIILHLNF
                               SLVGTPLSAFGNLRPVLAEDAQRLFTALFPFBKNCGNDNICQDDLSITFSFMSLDCLVVG
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completed: November 9, 2004, 12:47:03 he : 102.5 secs

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1 FNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSTGSCEPI 60
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99.9%; Score 5868; D
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1133; Conservative 3; Mismatches
                                                                                                                                                                                                                       ; Sequence 3, Application US/08173497; Patent No. 5437958; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1153 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1153 aming acid
                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
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CITY: Chicago
STATE: Illinois
COUNTRY: USA
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CLASSIFICATION:
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Appl
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Sequence 44, Appl
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                                                                                                       1 FNLDTENAMTFQENARGFGQ.....FKRQYKDMMSEGGPPGAEPQ 1137
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Sequence 43,
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(c) 1993 - 2004 Compugen Ltd.
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US-08-286-889-3
US-08-365-618-3
US-08-665-618-3
US-08-605-672-3
US-08-605-672-3
US-09-193-043-3
US-09-193-043-3
US-09-193-043-3
US-09-193-043-3
US-09-193-043-3
US-09-688-307A-3
US-09-350-259-3
US-08-476-062A-4
US-08-476-062A-44
US-08-476-062A-44
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US-08-286-889-4
US-08-485-618-4
US-08-362-652-4
US-08-605-672-4
US-08-482-293A-4
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US-08-286-889-2
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Maximum Match 100%
Listing first 45 summaries
                                 - protein search, using sw model
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length: 2000000000
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Match Length DB
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                                  OM protein
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Sequence 2, A Sequence 2, A Sequence 2, A Sequence 2, A Sequence 2, A Sequence 2, A Sequence 2, A Sequence 2, A Sequence 99, 1 Sequence 99, 1
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APPLICANT: Gallatin, W. Michael
APPLICANT: Van Der Vieren, Monica
TITLE OF INVENTION: No. 5437958el Human 2 Integrin Alpha
TITLE OF INVENTION: Subunit
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3: Marshall, O'Toole, Gerstein, Murray & Borun
233 S. Wacker Drive, 6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,497
US-08-485-618-2
US-08-362-652-2
US-08-362-652-2
US-08-482-293A-2
US-08-943-363-2
US-09-688-307A-2
US-09-350-259-2
US-08-482-293A-99
US-08-482-293A-99
US-08-943-363-99
US-09-193-043-99
US-09-193-043-99
US-09-350-259-99
US-09-350-259-99
US-09-350-259-95
US-09-350-259-95
                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: No. 5437958and, Greta E.
REGISTRATION NUMBER: 35,302
REPENCE/DOCKET NUMBER: 27866/31363
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
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1; Indels

DB 1; Length 1153;

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301 NFBALKTIQNQLREKIFALEGTQTGSSSFEHEMSQEGFSAALTSNGPLLSTVGSYDWAG 360
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                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
COMPATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,889
FILING DATE:
                                                                                                                                   E: Marshall, O'Toole, Gerstein, Murray
233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
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                Sequence 3, Application US/08286889
; Sequence 3, Application US/08286889
; Patent No. 5470953
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Mich
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5470953el Human 2
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 0;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 5868;
Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: P38,659
REFERENCE/POCKET NUMBER: 27866/32168
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 99.6%;
Matches 1133; Conservative 3
                                                                                                                                                                      CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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TOPOLOGY: lin
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RESULT 2
US-08-286-889-3
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                                                                             TDGBKFGDPLGYEDVI PEADREGVIRYVI GVGDAFRSEKSRQELNTIASKPPRDHVFQVN
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                      RLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLRQQPQK
                                                          PPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEF
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                PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                            NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
REFERNCE/DOCKET NUMBER: 27866/32797
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
APPLICATION UNBER: US 08/286,889
FILING DATE: 5-AUG-1994
APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
            SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
FILING DATE:
 PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                       : 1153 amino acids
amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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OPERATING SYSTEM:
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Matches 1133; Conserv
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                                                              QNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPL
                                                                                                                                            YDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNF
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233 South Wacker Drive, 6300 Sear Tower
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APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5728533el Human
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08485618 Patent No. 5728533
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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COUNTRY: United States
ZIP: 60606-6402
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STREET: 235
TTW: Chicago
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RESULT 3 US-08-485-618-3

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61 RLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLRQQPQK 120
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              27866/32391
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                            99.9<del>8</del>;
99.6<del>8</del>;
                                                                                         3
                                                                                                                       LENGTH: 1153 amino acids
TYPE: amino acid
                                          TELEFAX: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids
                                             : 312-474-6300
312-474-0448
                                                                                                                                                                                                                                        Best Local Similarity 99.6 Matches 1133; Conservative
                                                                                                                                                   STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                                                                                                                      SLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVG
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                                                  PVLRVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVT
                                                                     GPREFNVTVTVRNDGEDSYRIQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEV
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APPLICATION NUMBER: US/08/362,652
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08362652
Patent No. 5766850
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5766850el Human
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Chicago
STATE: 111inois
COUNTRY: United States
ZIP: 6666-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
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STREET: 233
CITY: Chica
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US-08-362-652-3
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                                                                                                                                                                                                                                  GPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEV
                       SGALKSTSCSINHPIPPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRINKTEF
                                     2 Integrin Alpha Subunit
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233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Version #1.25
                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08605672
Patent No. 5817515
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5817515el Human
NUMBER OF SEQUENCES: 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UNDRER: US 08/173,497
FILING DATE: 23-DEC-1993
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
FILING DATE: 5-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27866/32684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/605,672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 3:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM.
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-605-672-3
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                                            FNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSTGSCEPI
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     Score 5868;
Pred. No. 0
   99.9%;
Query Match
Best Local Similarity 99.6
Matches 1133; Conservative
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                                                              US-08-943-363-3
; Sequence 3, Application US/08943363
; Patent No. 5837478
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APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: NO. 5831029el Human
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TBLECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US/08/482,293A
FILING DATE:
CLASSIFICATION DATA:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/362,652
FILING DATE: 5-AUG-1994
PRIOR APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
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US-08-482-293A-3
; Sequence 3, Application US/08482293A
; Patent No. 5831029
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Matches 1133; Conservative
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INFORMATION FOR SEQ ID NO:
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APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
ITILE OF INVENTION: No. 6251395e1 Human 2
FILE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/193,043
CURRENT FILING DATE: 1998-11-16
EARLIER FILING DATE: 1993-12-23
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1994-12-21
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EARLIER FILING DATE: 1994-10-03
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                                                                              8: Marshall, O'Toole, Gerstein, Murray & Borun
233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                        ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 5868; D
Pred. No. 0;
3; Mismatches
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: NO. 5837478el Human
NUMBER OF SEQUENCES: 114
                                                                                                                                                                                                                                                                                               CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AGG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/943,363 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.98;
                                                                                                       CITY: Chicay
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
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INFORMATION FOR SEQ ID NO: 3:
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                                                                CORRESPONDENCE ADDRESS:
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MOLECULE TYPE: protein
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                                                                          ADDRESSEE: Mars
STREET: 233 SOU
CITY: Chicago
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Best Local Similarity
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NFEALKTIONOLREKIFALEGTOTGSSSSFEHEMSORGFSAALTSNGPLLSTVGSYDWAG 360
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                                              RINGTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDIP
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GREERAL INO. 0.4240.4

APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
FILE ARTEL CANTENTION: No. 6432404el Human Beta-2
FILE REFERENCE: 27866/36646
CURRENT APPLICATION NUMBER: 08/09/688,307A
CURRENT FILING DATE: 1998-11-16
FRIOR FILING DATE: 1998-11-16
FRIOR FILING DATE: 1996-02-2
FRIOR FILING DATE: 1996-02-2
FRIOR FILING DATE: 1994-08-05
FRIOR FILING DATE: 1994-08-05
FRIOR FILING DATE: 1994-08-05
FRIOR FILING DATE: 1994-12-21
FRIOR FILING DATE: 1994-12-21
FRIOR FILING DATE: 1994-12-21
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FRIOR FILING DATE: 1994-12-21
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FRIOR FILING DATE: 1997-10-03
FRIOR FILING DATE: 1997-10-03
FRIOR FILING DATE: 1994-12-21
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Pred. No. 0;
                                                                                                                                                                                                                                                                                  Sequence 3, Application US/09688307A Patent No. 6432404
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Best Local Similarity 99.6%;
Matches 1133; Conservative
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ORGANISM: ]
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                                                                                                                                       Length 1153;
                                                                                                                                                                    1; Indels
                                                                                                                                       DB 3;
                                                                                                                                      Score 5868; DB; Pred. No. 0; 3; Mismatches
                                                                                                                                         99.9%;
                                                                                                                                                                         Conservative
               NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patentin Ver. 2.
SEQ ID NO 3
LENGTH: 1153
                                                                       TYPE: PRT
) ORGANISM: Homo sapiens
US-09-193-043-3
                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                         Matches 1133;
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GPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEV GPREFNVIVIVANDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEV SCALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRTNKTEF

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Sequence 3, Application US/09350259 Patent No. 6620915

FALCELL WO. 9020313 GRENEAL INFORMATION: APPLICANT: Gallatin, Michael W. APPLICANT: Gallatin, Michael W. TITLE OF INVENTION: NO. 662091561 Human 2 FILE REFRENCE: 27866/35004 CURRENT APPLICATION NUMBER: US/09/350,259 CURRENT FILING DATE: 1999-07-08 EARLIER APPLICATION NUMBER: 09/193,043 EARLIER FILING DATE: 1999-11-16 EARLIER FILING DATE: 1993-12-23 EARLIER FILING DATE: 1994-08-05 EARLIER FILING DATE: 1994-08-05

; EARLIER FILING DATE: 1994-12-21
; EARLIER APPLICATION NUMBER: 08/943,363
; EARLIER FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1153
; TYPE: PRT ; ORGANISM: Ho US-09-350-259-3

ó 136 120 180 240 196 256 300 360 376 420 316 9 16 TDGEKFGDPLGYEDVIPEADREGVIRYVIGYGDAFRSEKSRQELNTIASKPPRDHVFQVN NFEALKTIONOLREKIFAIEGTQTGSSSSFEHEMSOEGFSAAITSNGFLLSTVGSYDWAG FNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDXSTGSCEPI RLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLRQQPQK PPBALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEF RIHFTFKEFQNNPNPRSLVKPITQLLGRTHTATGVRKVIRELLNITNGARKNAFKILIVI GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR Gaps ·, Length 1153; Indels 1; ., DB Pred. No. 0; 3; Mismatches Score 5868; 99.98; Conservative Query Match Best Local Similarity Matches 1133; Conserv н 61 137 197 121 181 241 301 361 à q ò ag y qq à QQ ठे g à g d à

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| Db 957 SGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMFRTNKTEF 916 | 917 QLELPVKYAVYWVTSHGVSTKYLNFTASENTSRVMQHQYQVSNLGQRSLPISLVFLVP          | Qy 961 RINQTVIMDRPQVTFSENLSSTCHIKEKLPSHSDFLMELKAPVNICSTAVCKELQCLF 1020<br> | Qy 1021 FFGIQBEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFWDSVFTLLPGQGAFVRSQTET 1080   | 113  | Db 1097 KVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMMSEGGPPGAEPQ 1153 | RESULT 11<br>US-08-476-062A-43<br>; Sequence 43, Application US/08476062A<br>: Parent No. 5877275 | GENERAL INFORMATION: APPLICANT: Armaout, M. Amin TITLE OF INVENTION: CONTROLLING CELLULAR IMMUNE/INFLAMMATORY TITLE OF INVENTION: RESPONSES WITH BETA2 INTEGRINS | NUMBER OF SEQUENCES: 53 CORRESPONDENCE ADDRESS: ADDRESSEB: Fish & Richardson P.C. STREET: 2.5 Franklin Street | ; CITY: Boston<br>; STATE: MA<br>; COUNTY: US                        | COMPUTER READABLE FORM:  COMPUTER READABLE COMPUTER: IBM Comparatible COPPUTER: IBM Comparatible COPPUTER: IMM Comparatible | SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/476,062A FILING DATE: 07-UIN-1995 | PRIOR APPLICATION DATA:  APPLICATION NUMBER: 08/216,081  FILING DATE: 21-MAR-1994  ADDITION NUMBER: 07/637.830 | FILING DATE: 04-JAN-1991<br>  APPLICATION NUMBER: 07/539,842<br>  FILING DATE: 18-JUN-1990<br>  APPLICATION NUMBER: 07/212.573 | 1988<br>TION:<br>W.  | REFERENCE/DOCKET NUMBER: 00786/068003<br>  TELECOMMUNICATION INFORMATION:<br>  TELEPHONE: 617/542-5070<br>  TELEPAX: 617/542-8906 | 25.4   | # 25.55   | A-43<br>Similar<br>D; Con  |

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                                      GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR
                                                                  377 GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR
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APPLICANT: ARNAOUT, M. AMIN

ITILE OF INVENTION: HUMAN CR3a/D HETERODIMERS

NUMBER OF SEQUENCES: 12

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 105/08/78,871

FILING DATE: 16-JUN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 239,842

FILING DATE: 18-JUN-1990

APPLICATION NUMBER: 212,573

FILING DATE: 28-JUN-1988
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225 Franklin Street
                                                                                                                                     Sequence 43, Application PC/TUS9601314 GENERAL INFORMATION:
                                                                                                                                                                                                             FOR
                                                                                                                                                                                 APPLICANT: M. Amin Arnaout
TITLE OF INVENTION: METHODS FOR
TITLE OF INVENTION: ANTAGONISTS
NUMBER OF SEQUENCES: 78
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REFRENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-8906
TELEFAX: (617) 542-8906
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Best Local Similarity 99.4
Matches 1130; Conservative
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                         Massachusetts
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STATE: Massachu
COUNTRY: U.S.A.
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                                                                                          RESULT 12
PCT-US96-01314-43
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PCT-US96-01314-43
                          1096
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                                                                                                                                                                                                                                                                       APPLICANT: Arnaout, M. Amin
TITLE OF INVENTION: CONTROLLING CELLULAR IMMUNE/INFLAMMATORY
TITLE OF INVENTION: RESPONSES WITH BETA2 INTEGRINS
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
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59.1%; Score 34/3; 
Best Local Similarity 61.3%; Pred. No. 4.2e
Matches 692; Conservative 138; Mismatches
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                         Sequence 44, Application US/08476062A Patent No. 5877275 GENERAL INFORMATION:
APPLICANT: Arnaout, M. Amin
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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-08-476-062A-44
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STATE: M.
COUNTRY:
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                                                                                                               FNLDTENAMTFQENARGFGGSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSTGSCEPI
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                                   3;
           Pred. No. 0;
3; Mismatches
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                                     Conservative
                Best Local Similarity
                                   Matches 1130;
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                                                                301 NFBALKTIQNQLREKIFAIEGTQTGSSSSFEHEMSQEGFSAAITSNGPLLSTVGSYDWAG 360
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                                                                                                                                                                                 PRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLF
                                                                                                                                                                                                                                                          PVLRVKAIMEFNPREVARNVFECNDQVVKGKEAGEVRVCLHVQKSTRDRLREGQIQSVVT
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Sequence 44, Application PC/TUS9601314
GENERAL INFORMATION:
APPLICANT: M. Amin Arnaout
TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN
TITLE OF INVENTION: ANTAGONISTS
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS: RESULT 15 PCT-US96-01314-44

61 RLQVPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLRQQPQK 120 TDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVN 300 20 FNLDTEELTAFRVDSAGFGDSVVQYANSWVVGAPQKITAANQTGGLYQCGYSTGACFPI PPEALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEF 301 NFEALKTIONQLREKIFALEGTOTGSSSSFEHEMSQEGFSAAITSNGPLLSTVGSYDWAG RIHFTFKEFQNNPNPRSLVKPITQLLGRTHTATGVRKVIRELLNITNGARKNAFKILIVI : ||||:||: || || ||: || ||:|| ||:||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: | GVFLYTSKEKSTFINMTRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFR 421 QNTGMMESNANVKGTQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPL 1 FNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVAANQRGSLYQCDYSTGSCEPI PRGQRARWQCDAVLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLF Gaps 9 Length 1163; Indels Query Match
Best Local Similarity 61.3%; Pred. No. 4.ze-20.,
Matches 692; Conservative 138; Mismatches 293; COUNTY: U.S.A.

ZIF: 0110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordberfect (Version 5.1)
CURRENT APPLICATION NUMBER: PCT/US96/01314
FILING DATE: 30-JAN-96
PRICATION NUMBER: 08/380,167
FILING DATE: 30-JAN-95
ATTORNEY/AGENT INFORMATION: 00786/267001 225 Franklin Street NAME: John W. Freeman REGISTRATION NUMBER: 29,066 REFERENCE/DOCKET NUMBER: 00 TELECOMMUNICATION: INFORMATION: (617) 542-5070 (617) 542-8906 TELEX: 200154 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: Massachusetts TYPE: amino acid STRANDEDNESS: Boston 1163 ADDRESSEE: STREET: 22 TELEPHONE: ; TOPOLOGY: PCT-US96-01314-44 TELEFAX: TELEX: 20 LENGTH: 121 241 258 361 438 181 318 181 Ωp à 엄 à 셤 δ qq ò ద δ g ò g ð Dp ð

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420 437 480 497

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                                                                                                                                                                                                                                              960 VRINOTVIWDRPQVIFSENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQRIQCDI 1019
                                                                                                                                                                                                                                                                                           SGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLLKANVTSENNMPRINKTEF 900
                                  SLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVG 780
                                                                                                                781 GPREFNVTVTVRNDGEDSYRTQVTFFFPLDLSYRKVSTLQNQRSQRSWRLACESASSTEV 840
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661 YDLALDSGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNF
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Search completed: November 9, 2004, 12:21:14 Job time : 28 secs